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(54) **POLYPEPTIDE INDUCING APOPTOSIS**
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(57) **ABSTRACT**

This invention relates to reconstructed polypeptides which have properties of inducing apoptosis of nucleated blood cells having Integrin Associated Protein (IAP) and causing no hemagglutination. The reconstructed polypeptides comprise two or more H chain V regions and two or more L chain V regions of a monoclonal antibody which induces apoptosis of nucleated blood cells having IAP. The reconstructed polypeptides are useful as a therapeutic agent for blood dyscrasia such as leukemia.

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Fig. 1

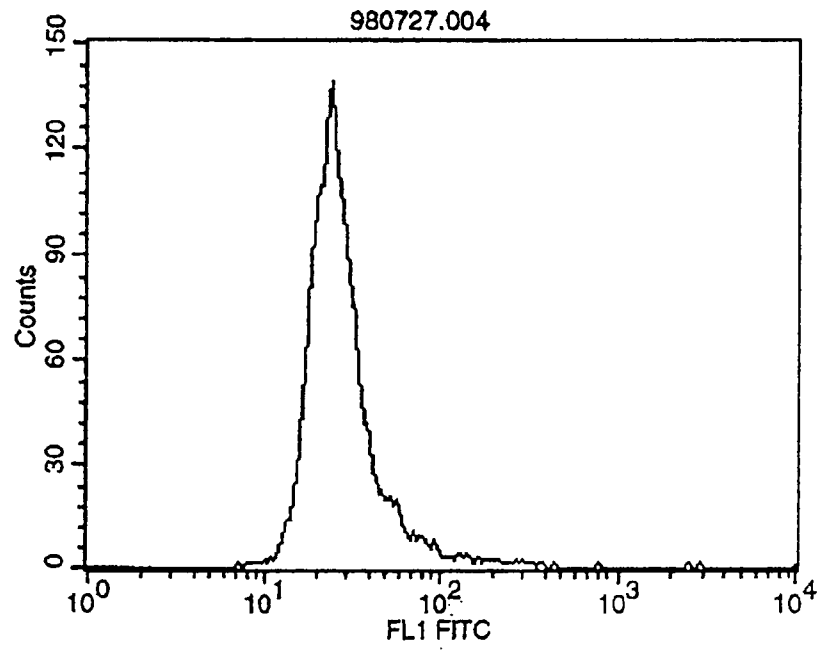


Fig. 2

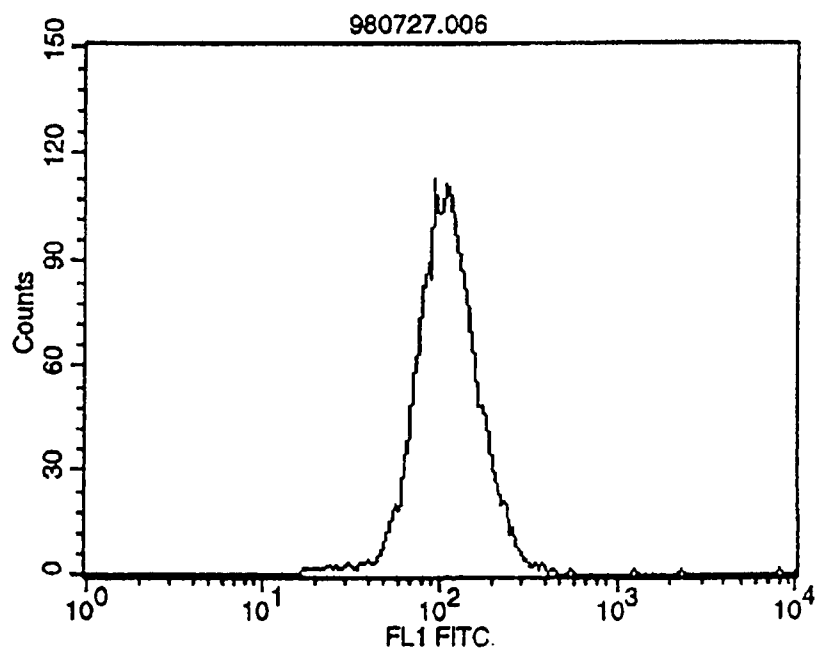


Fig. 3

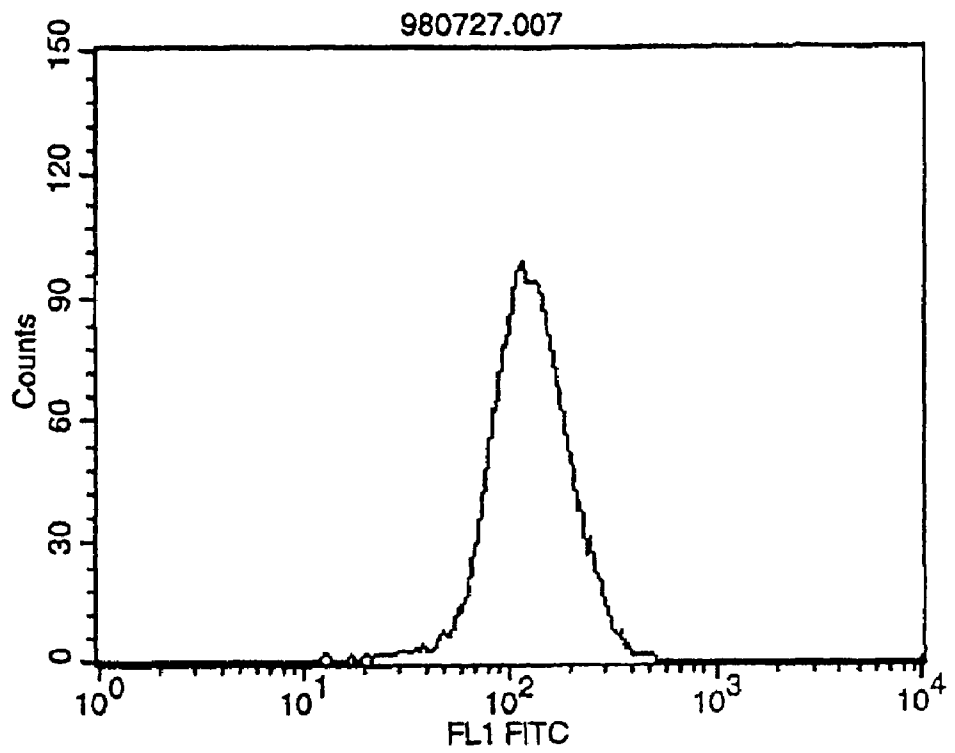


Fig. 4

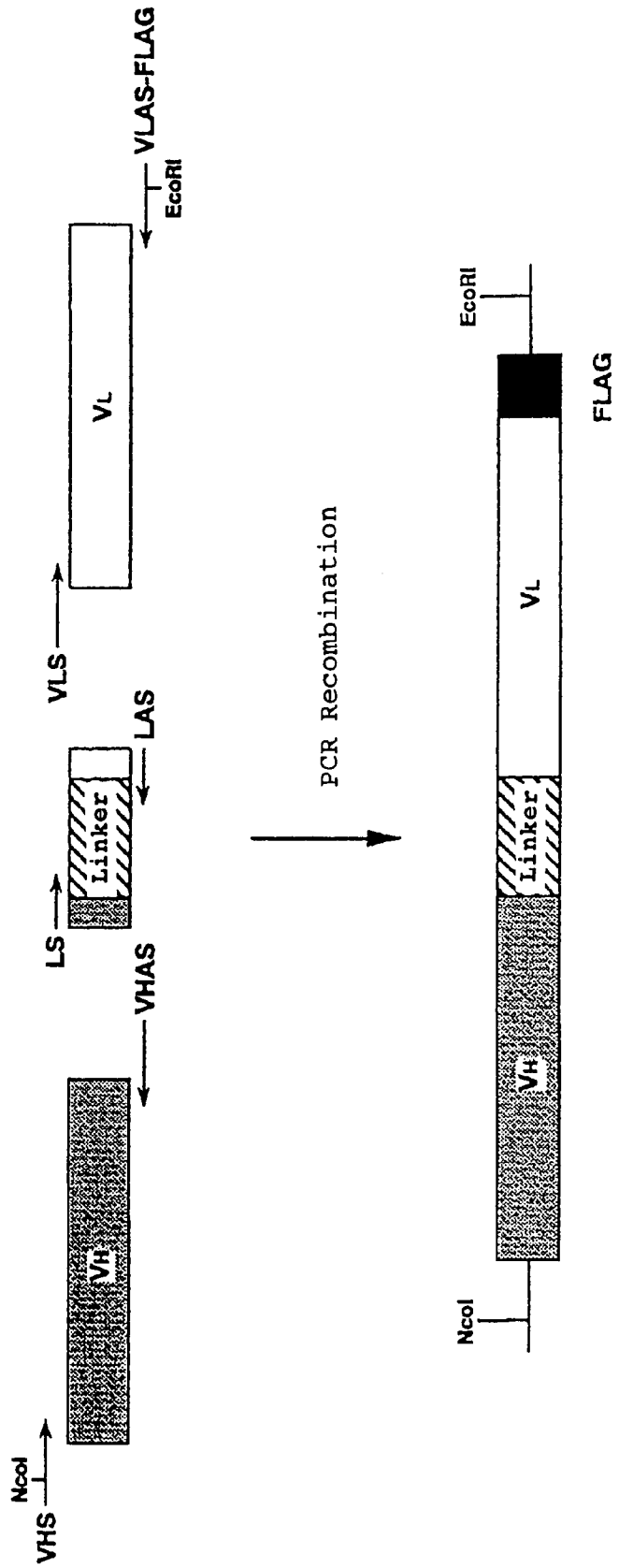


Fig. 5

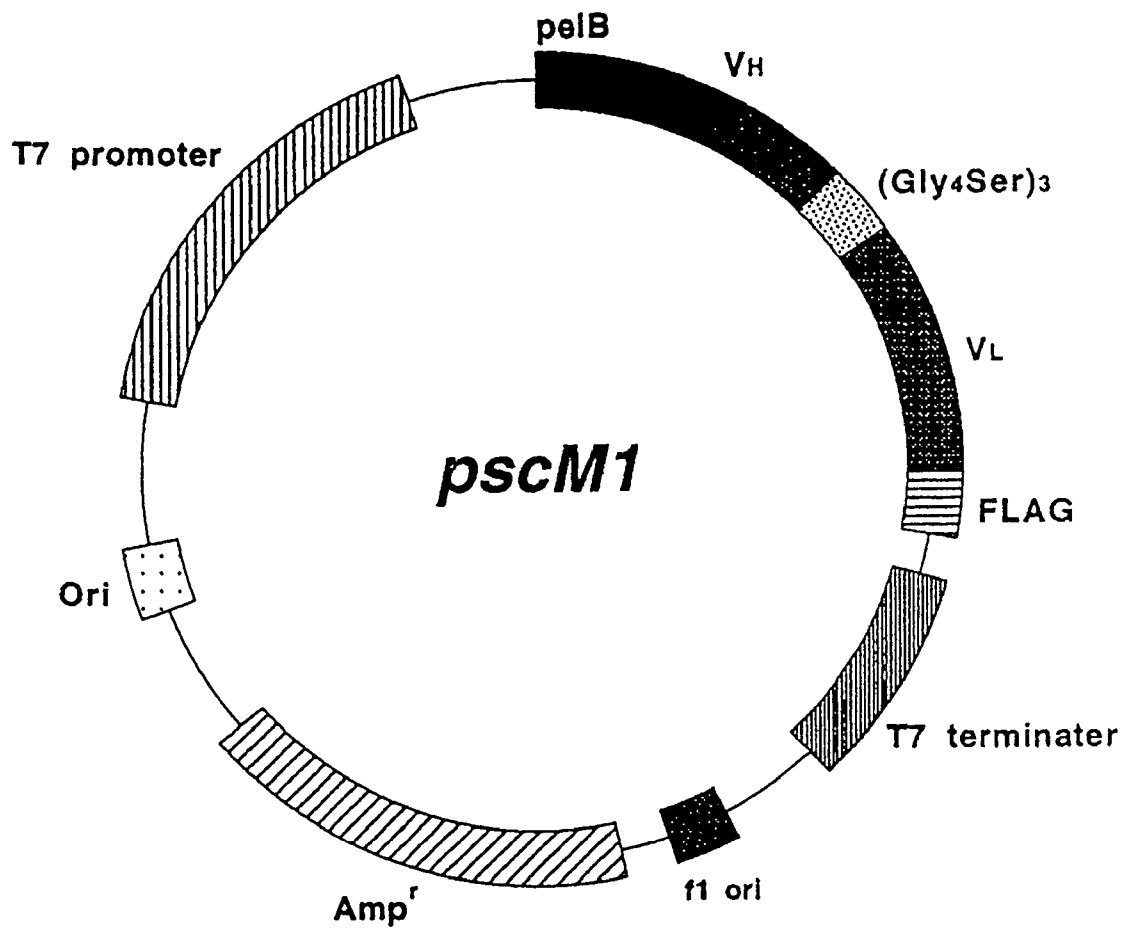


Fig. 6

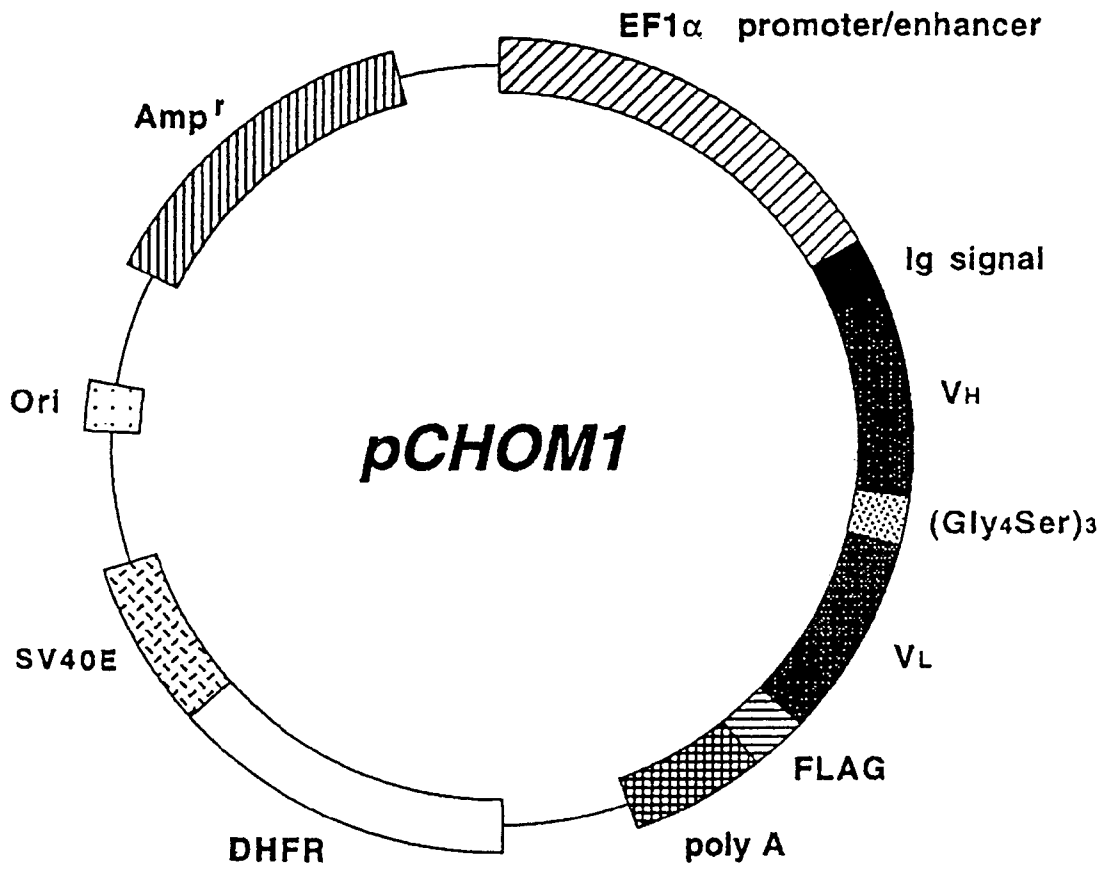


Fig. 7

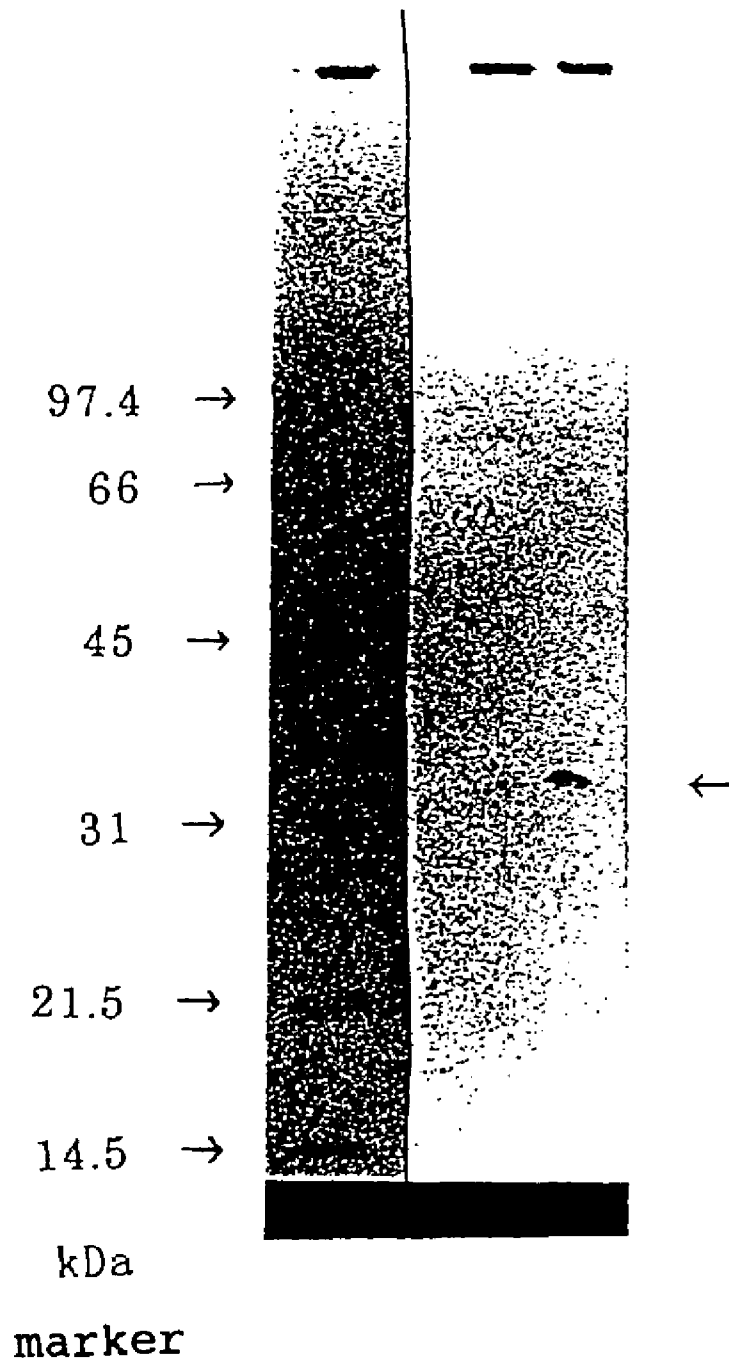


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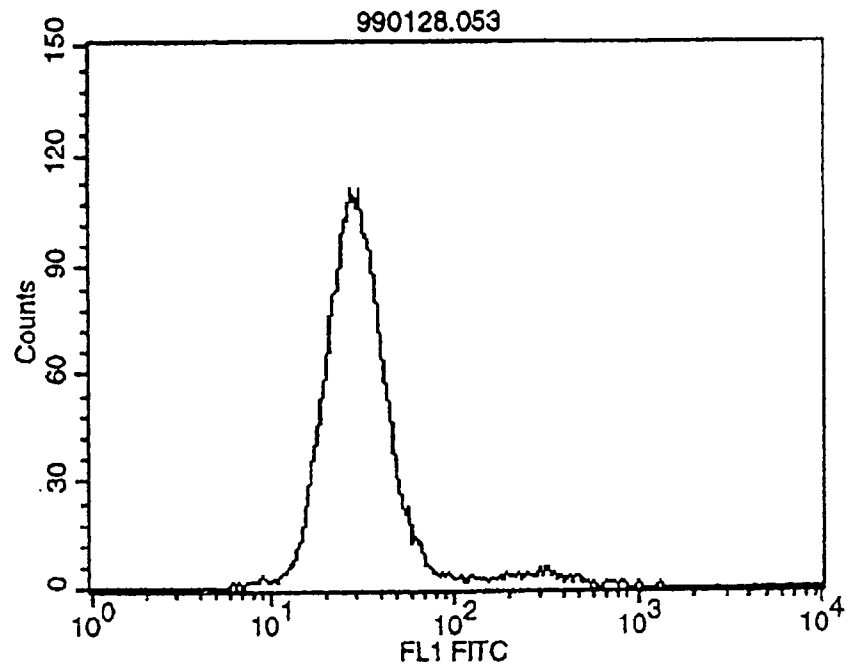


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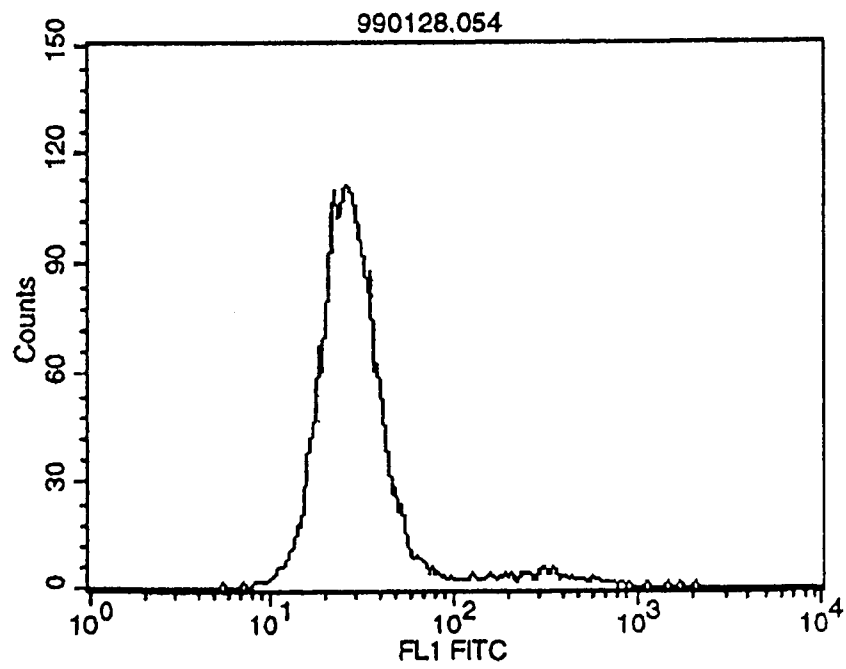


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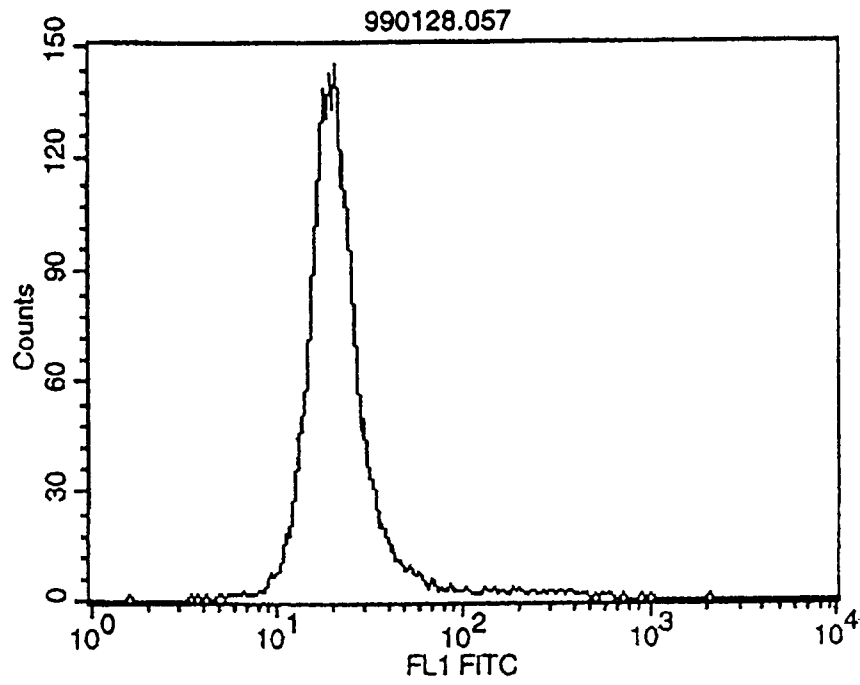


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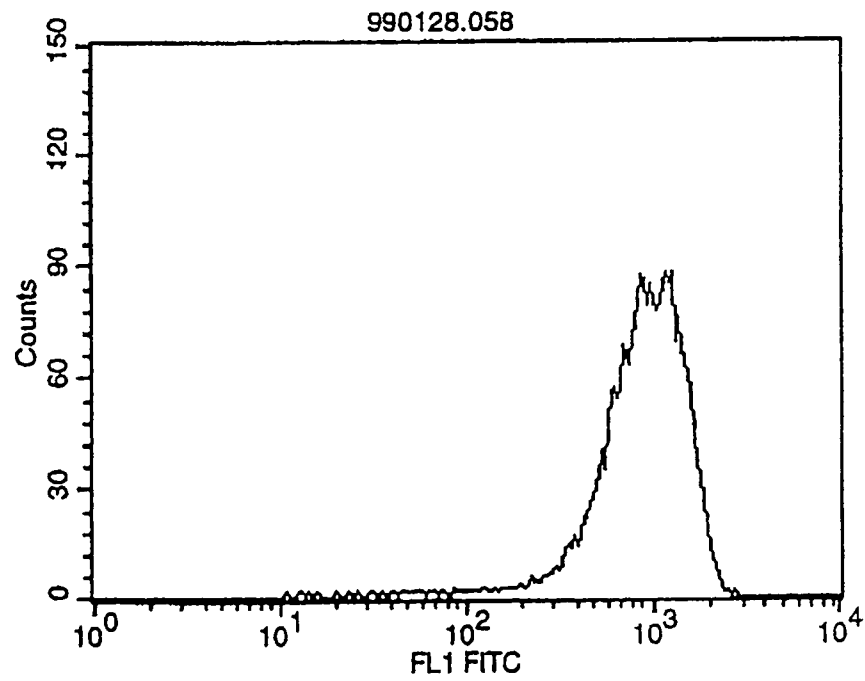


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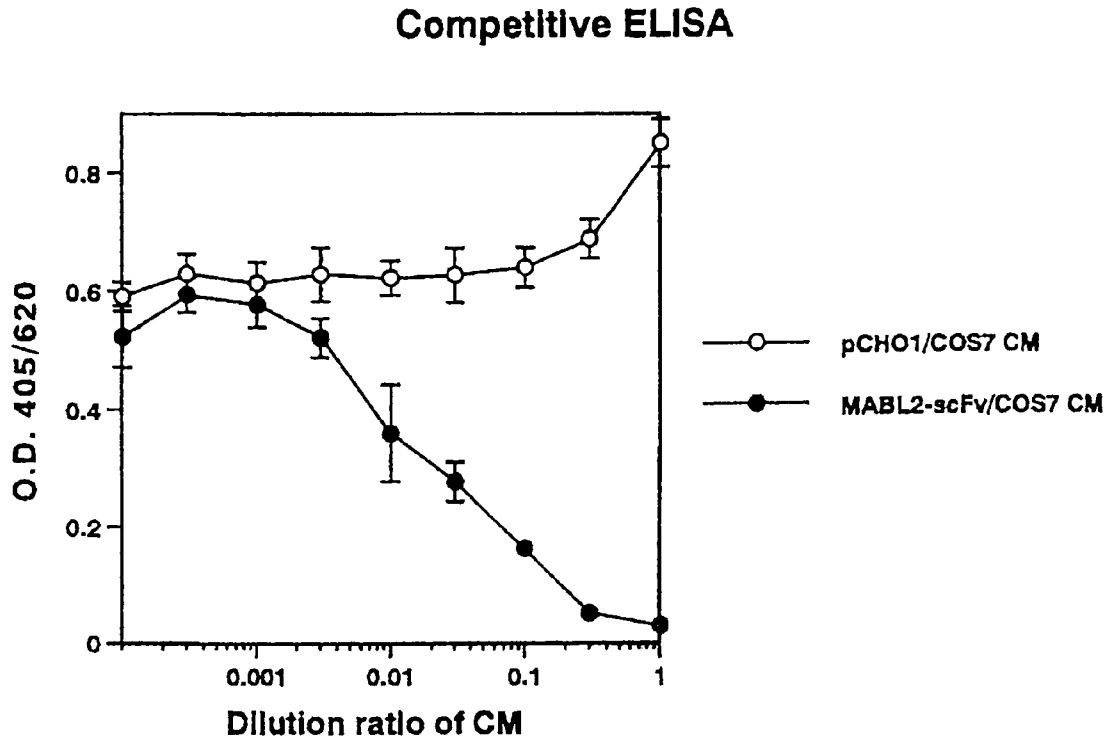


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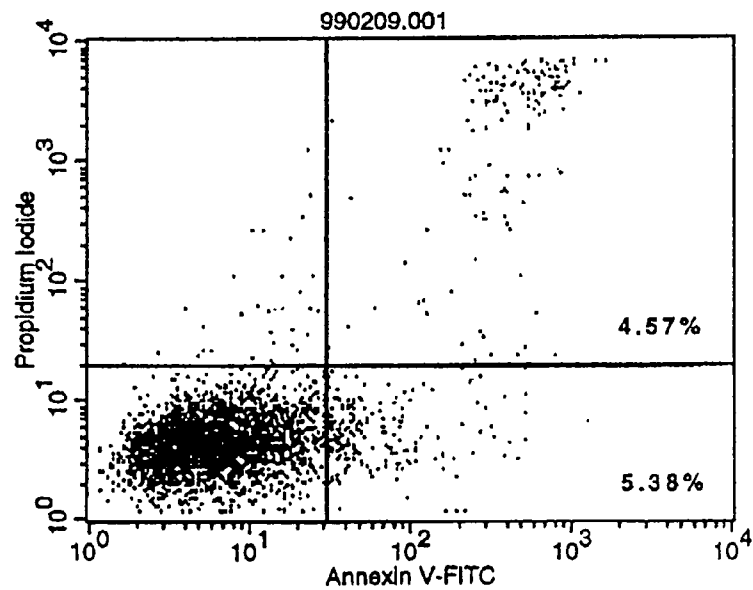


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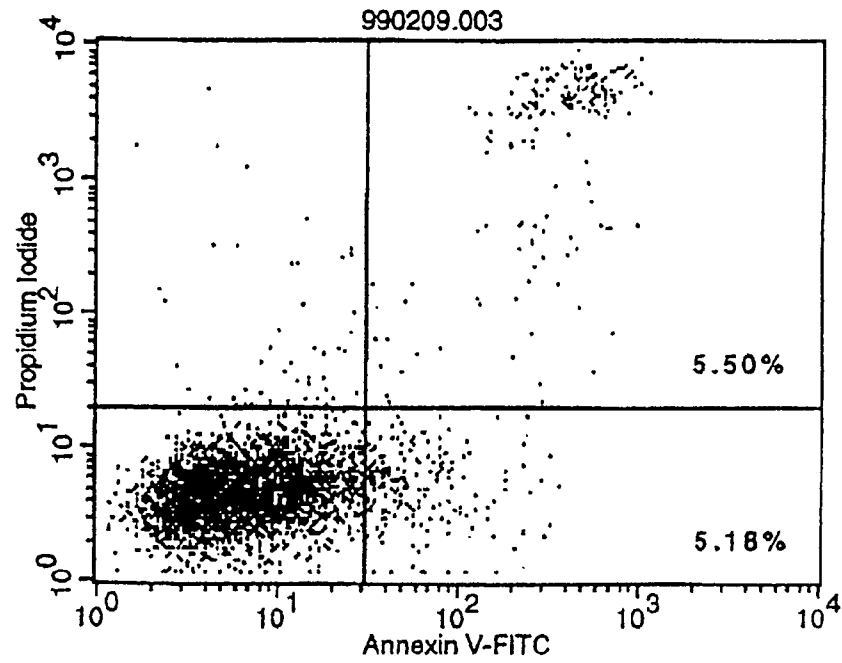


Fig. 15

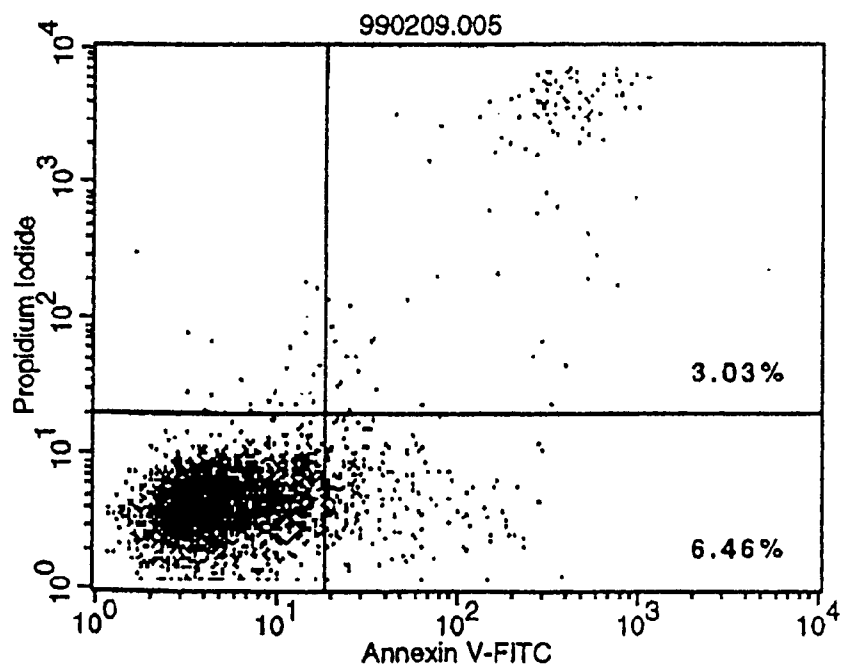


Fig. 16

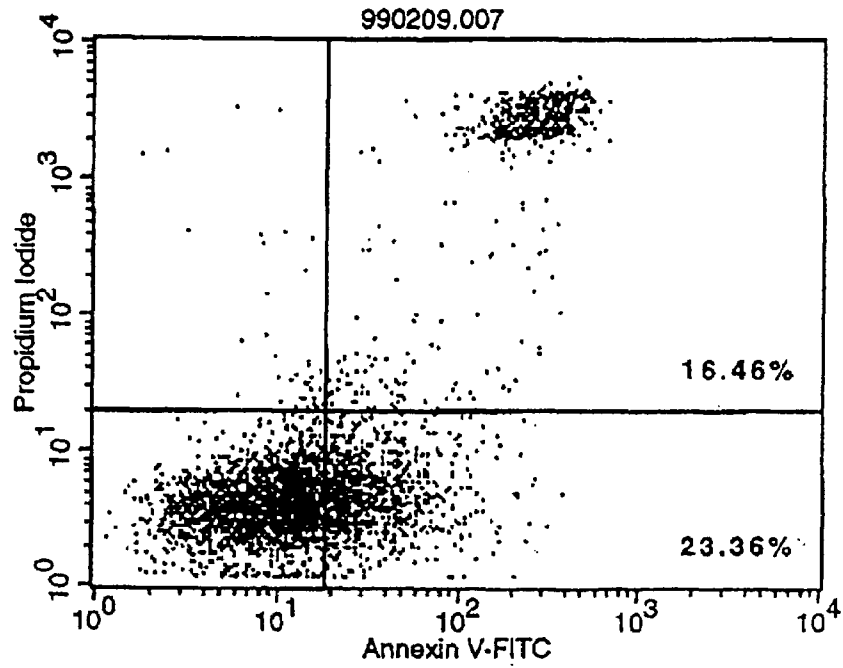


Fig. 17

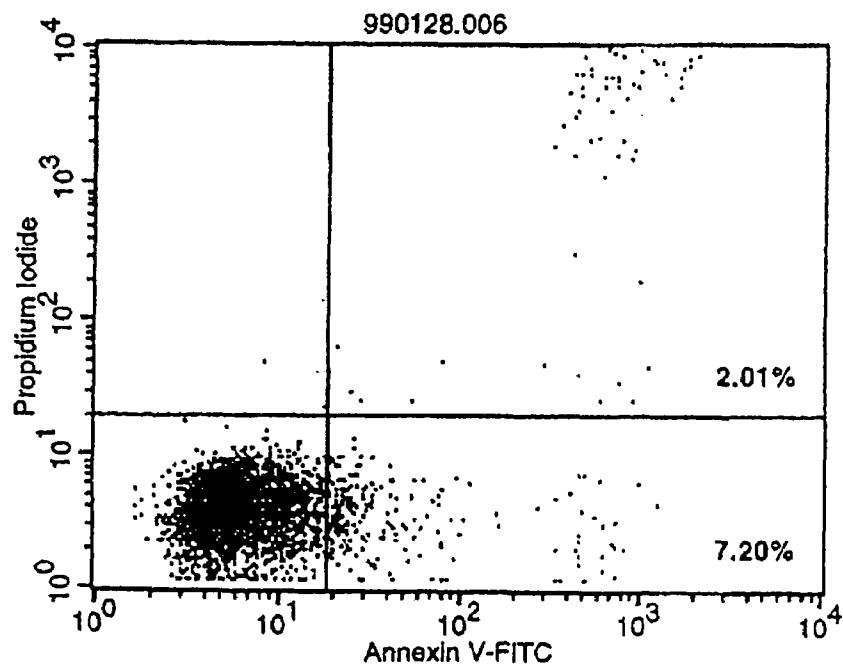


Fig. 18

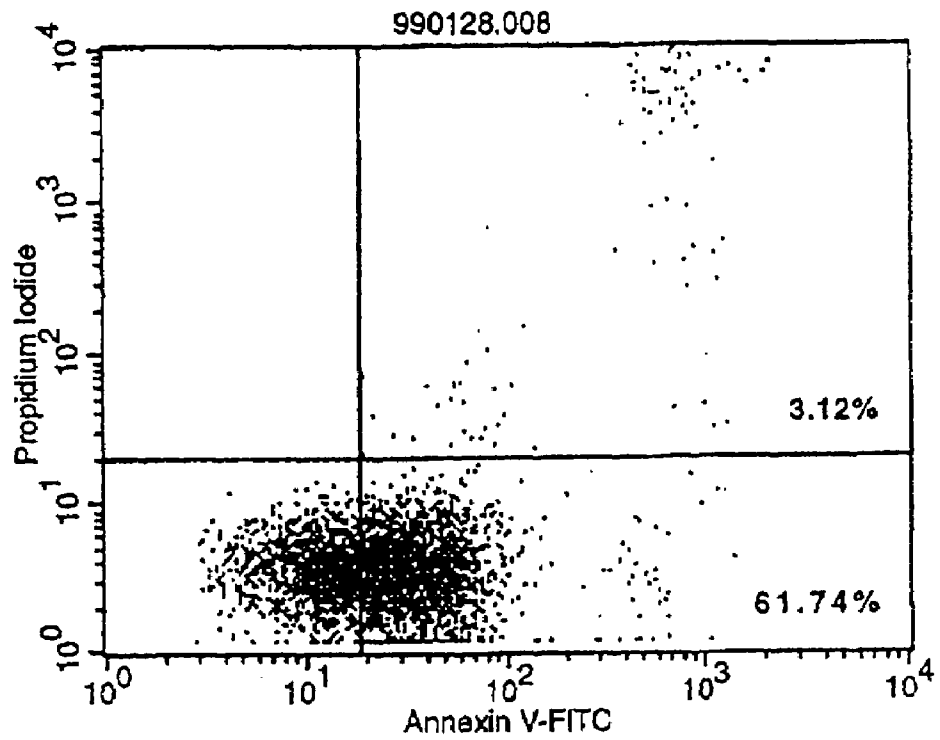


Fig. 19

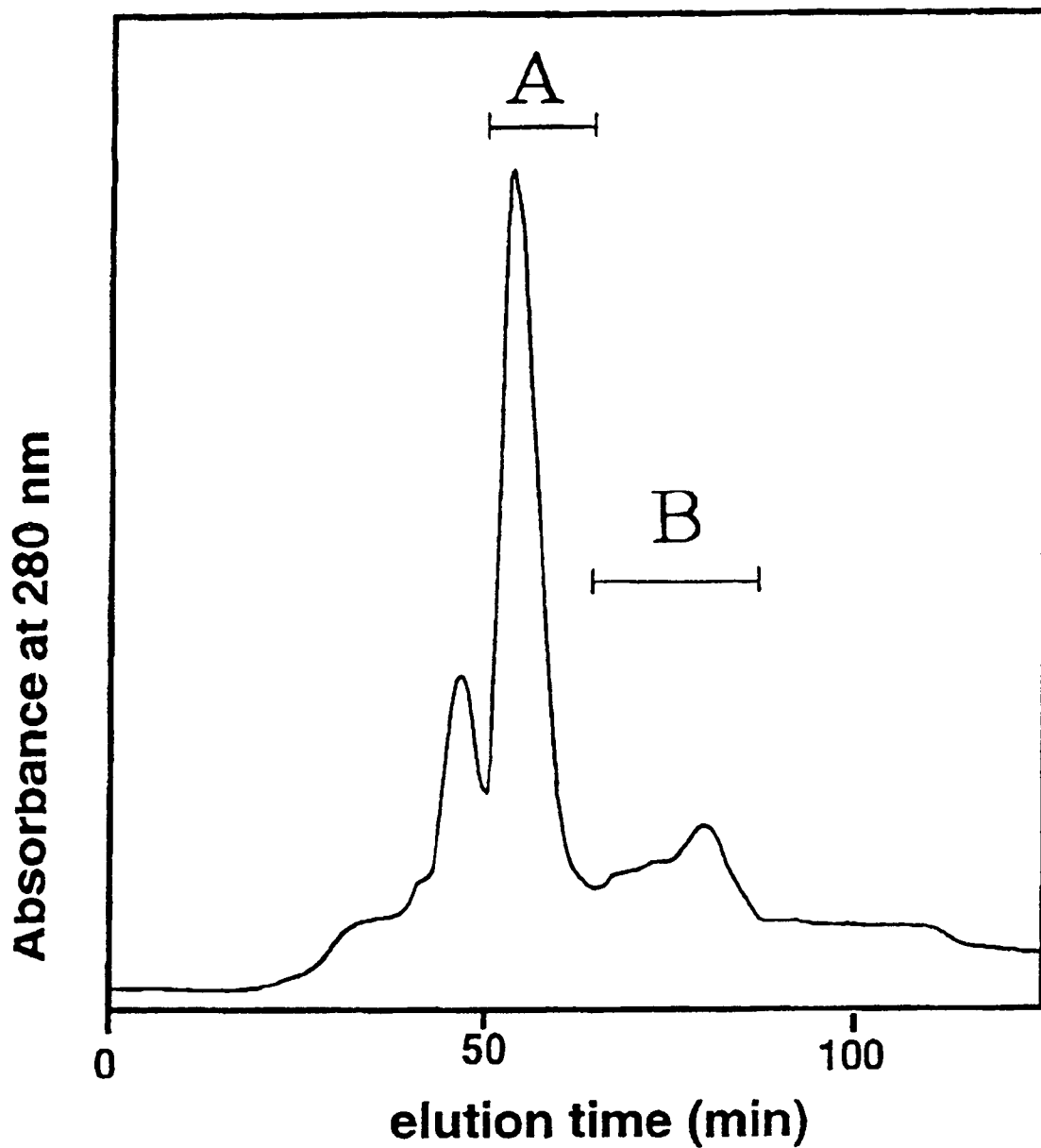


Fig. 20

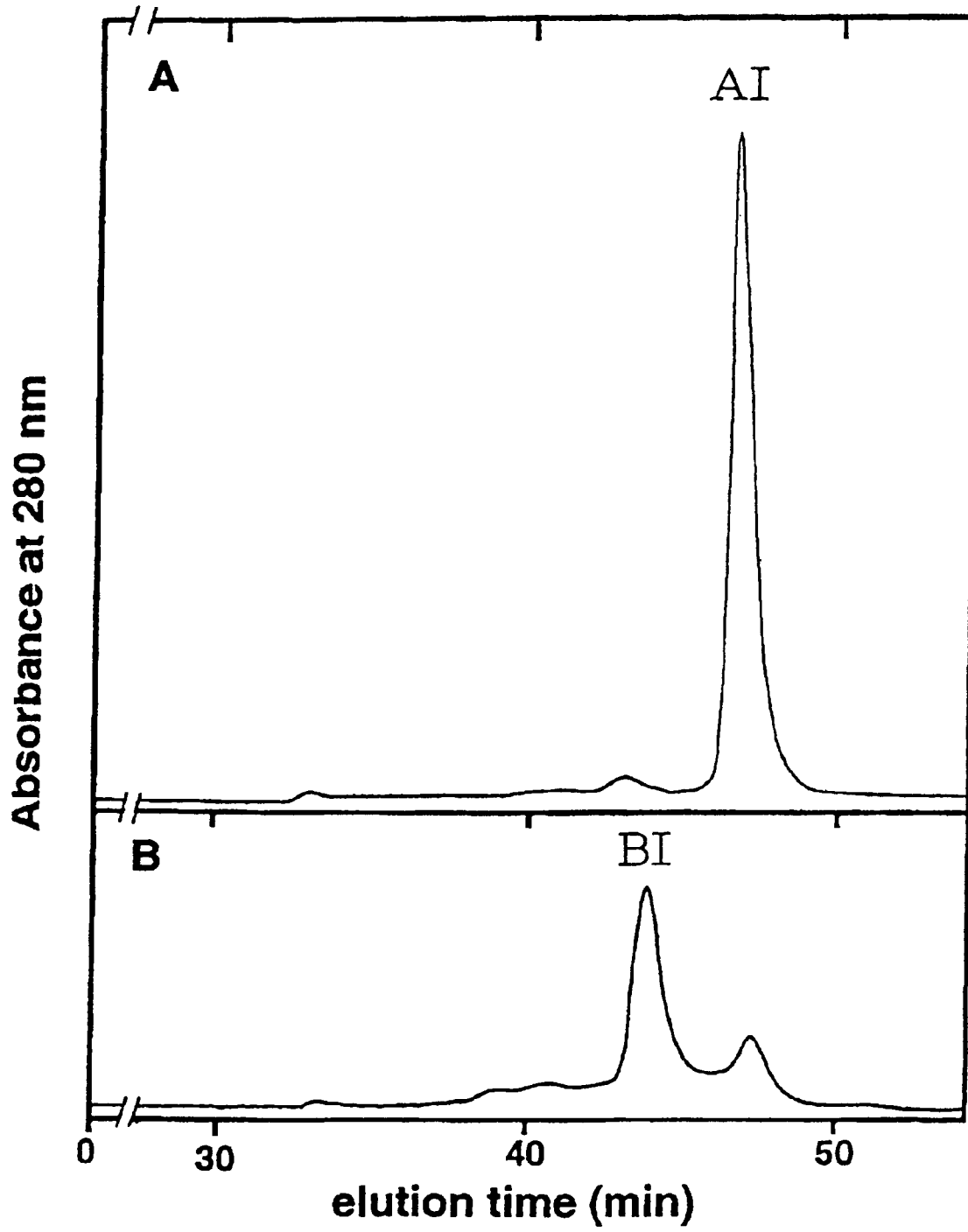


Fig. 21

SDS-PAGE analysis of MABL2-scFv

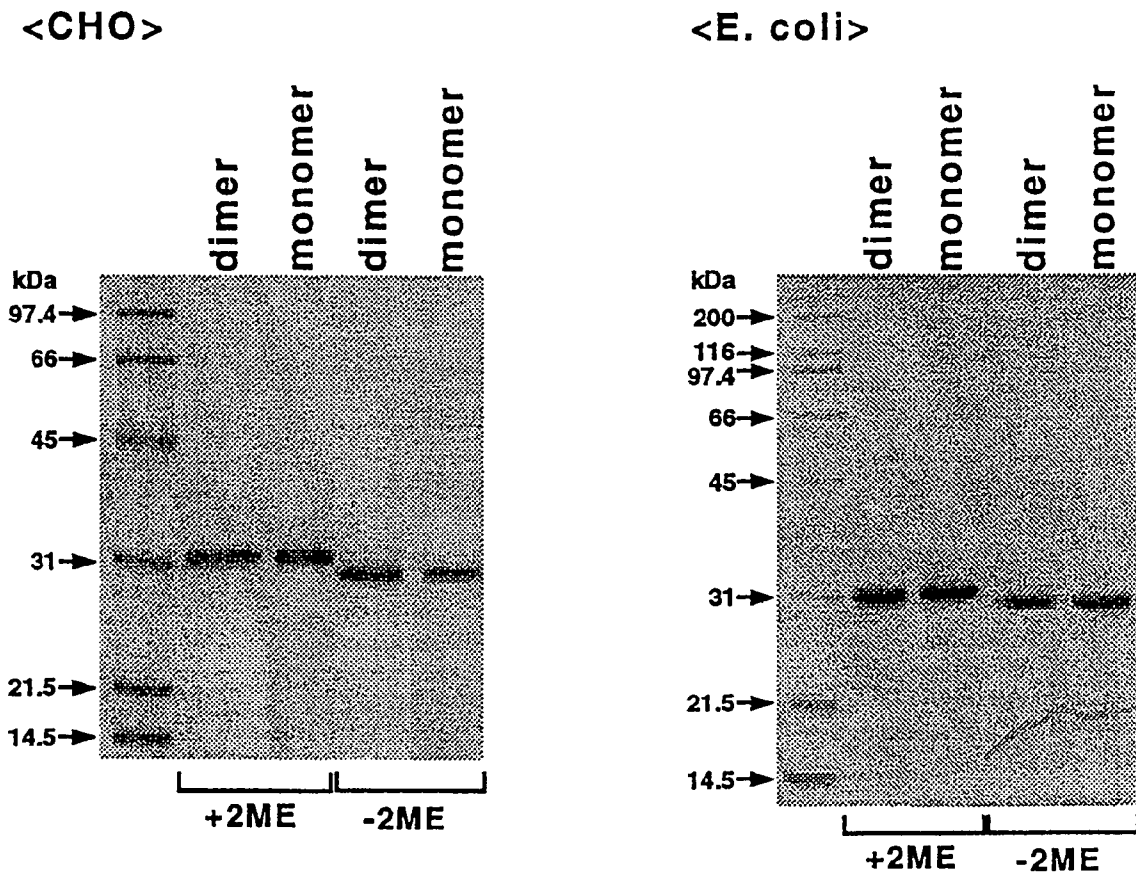


Fig. 22

TSK gel G3000SW

20 mM Acetate buffer, 0.15 M NaCl, pH 6.0

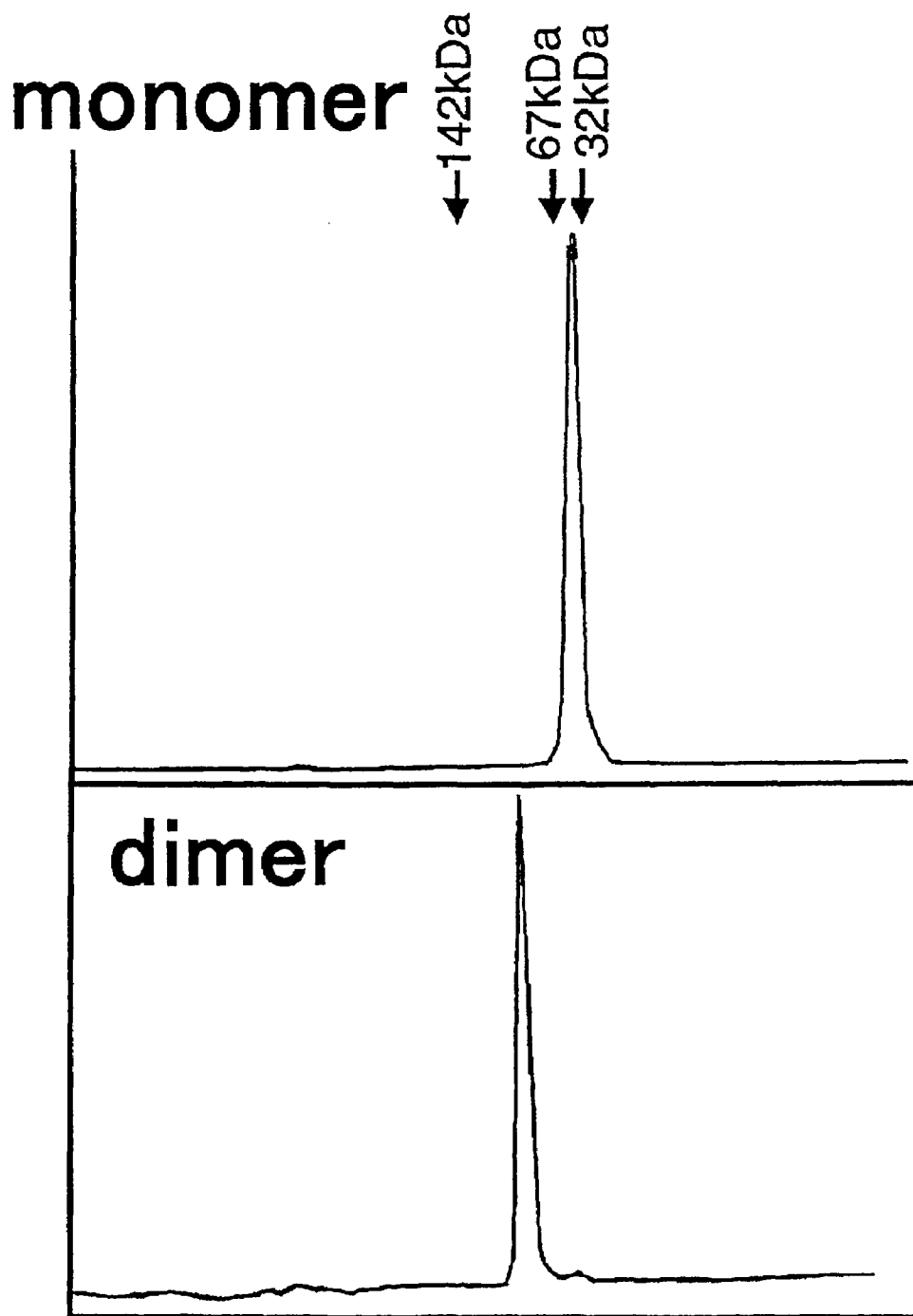


Fig. 23

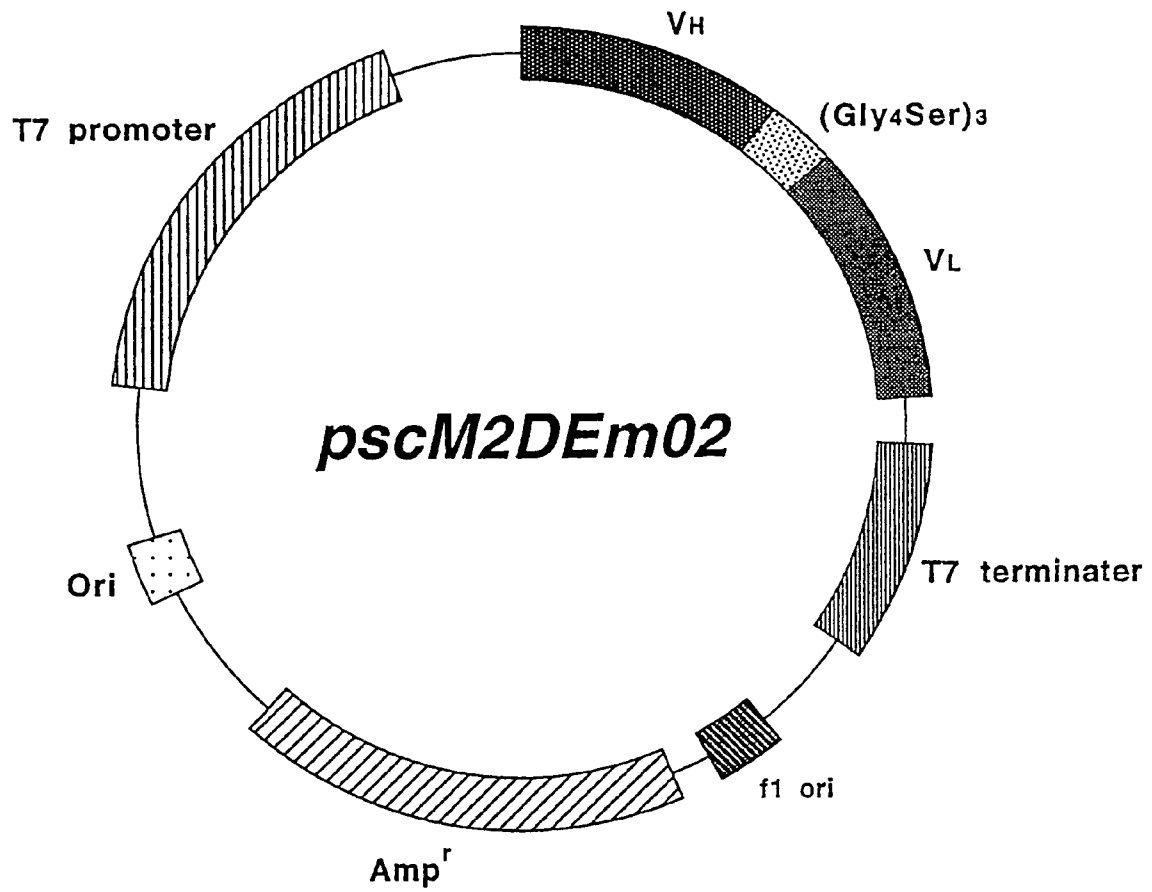


Fig. 24

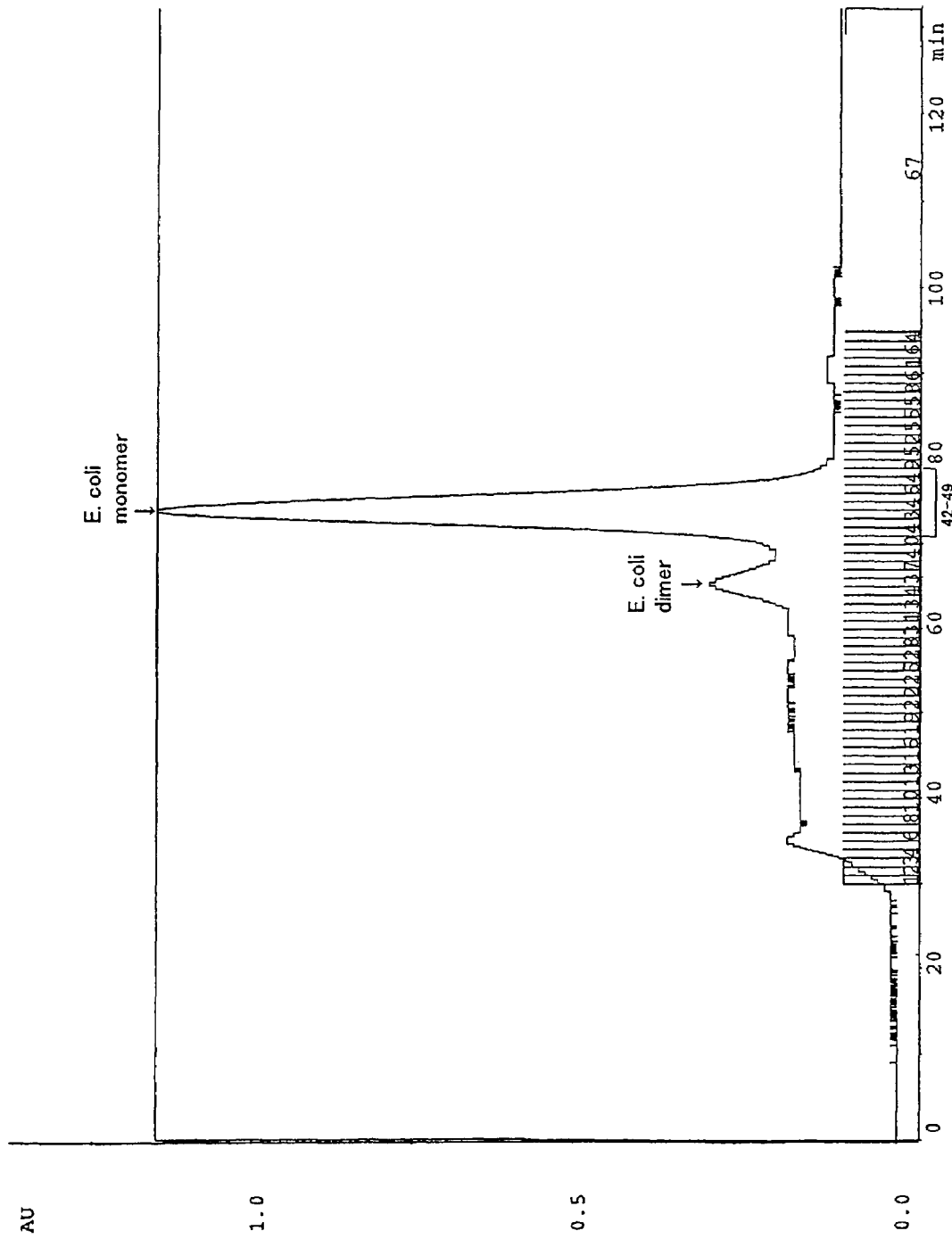


Fig. 25

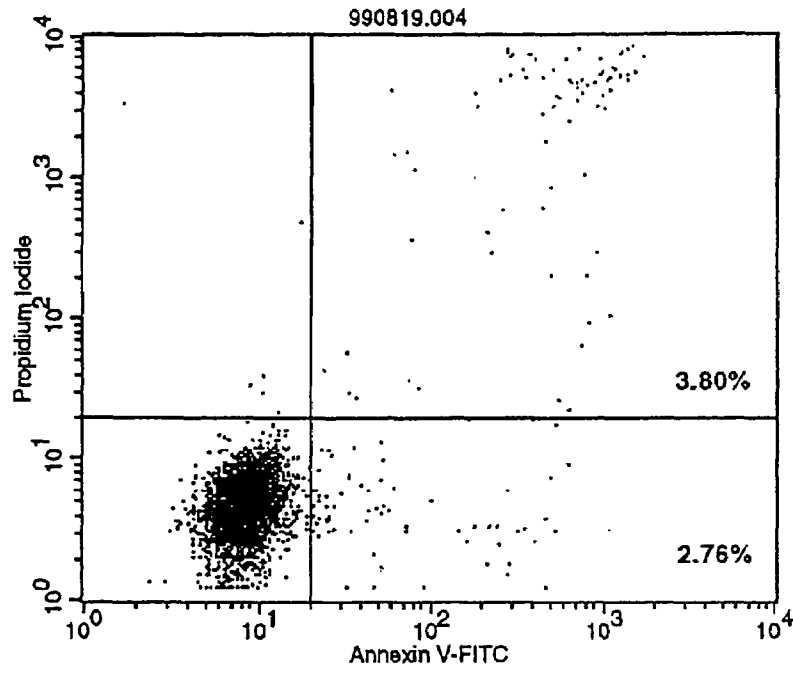


Fig. 26

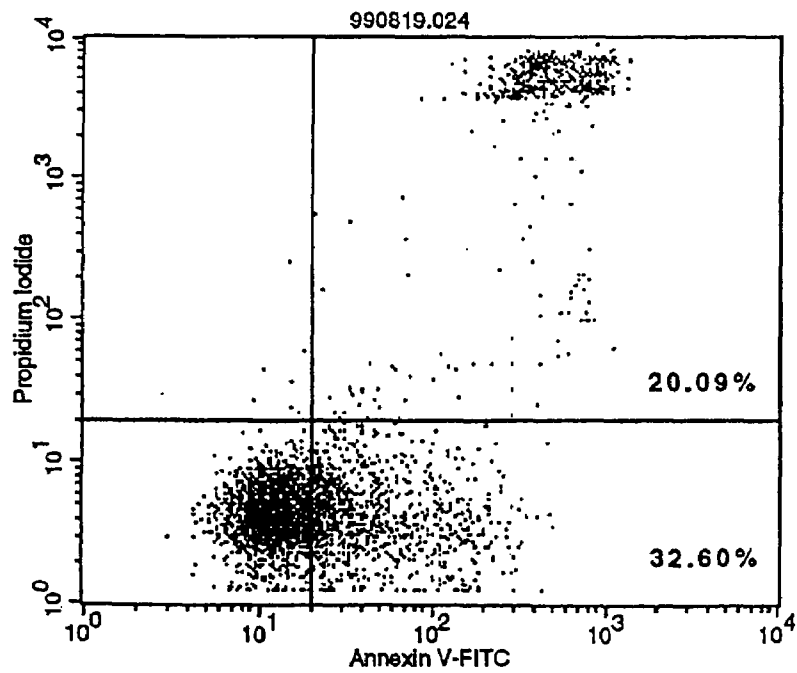


Fig. 27

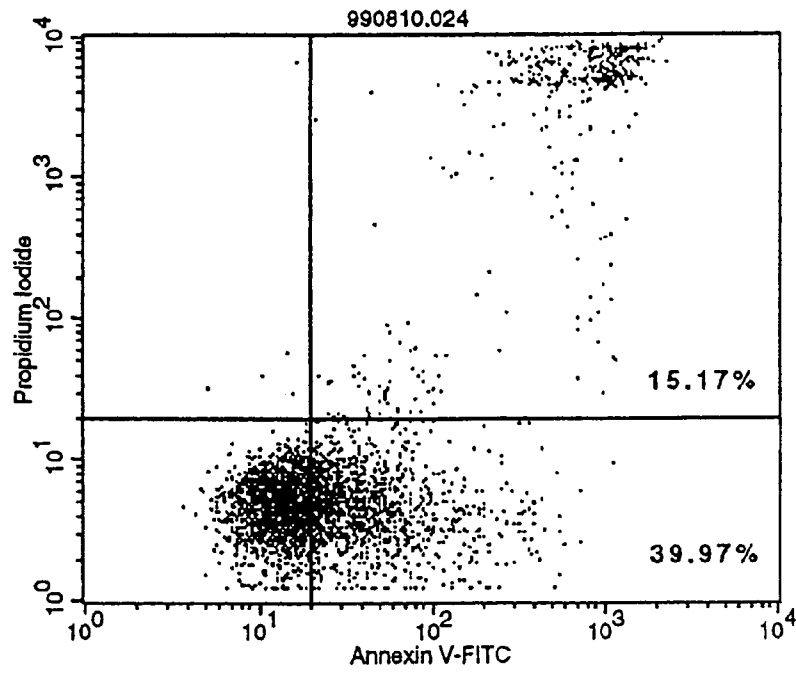


Fig. 28

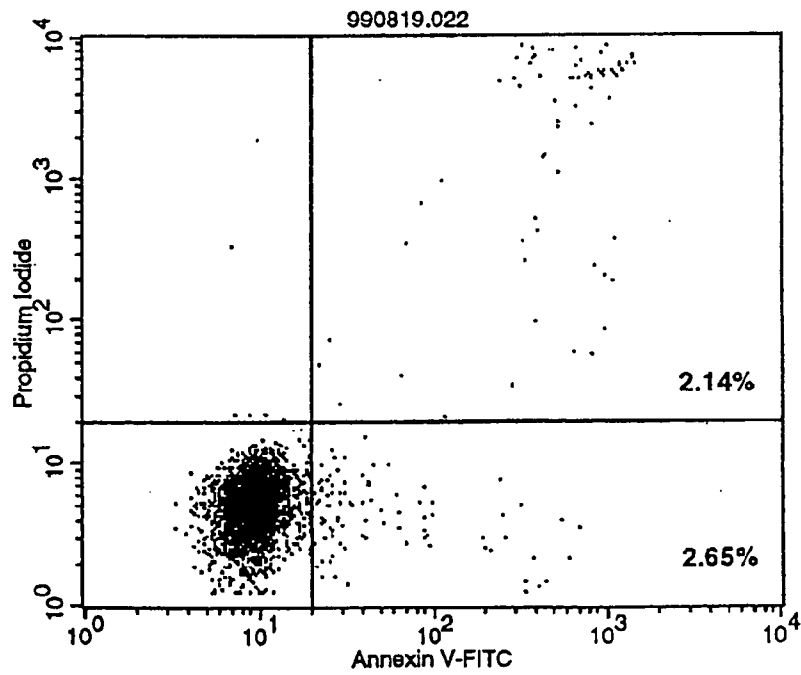


Fig. 29

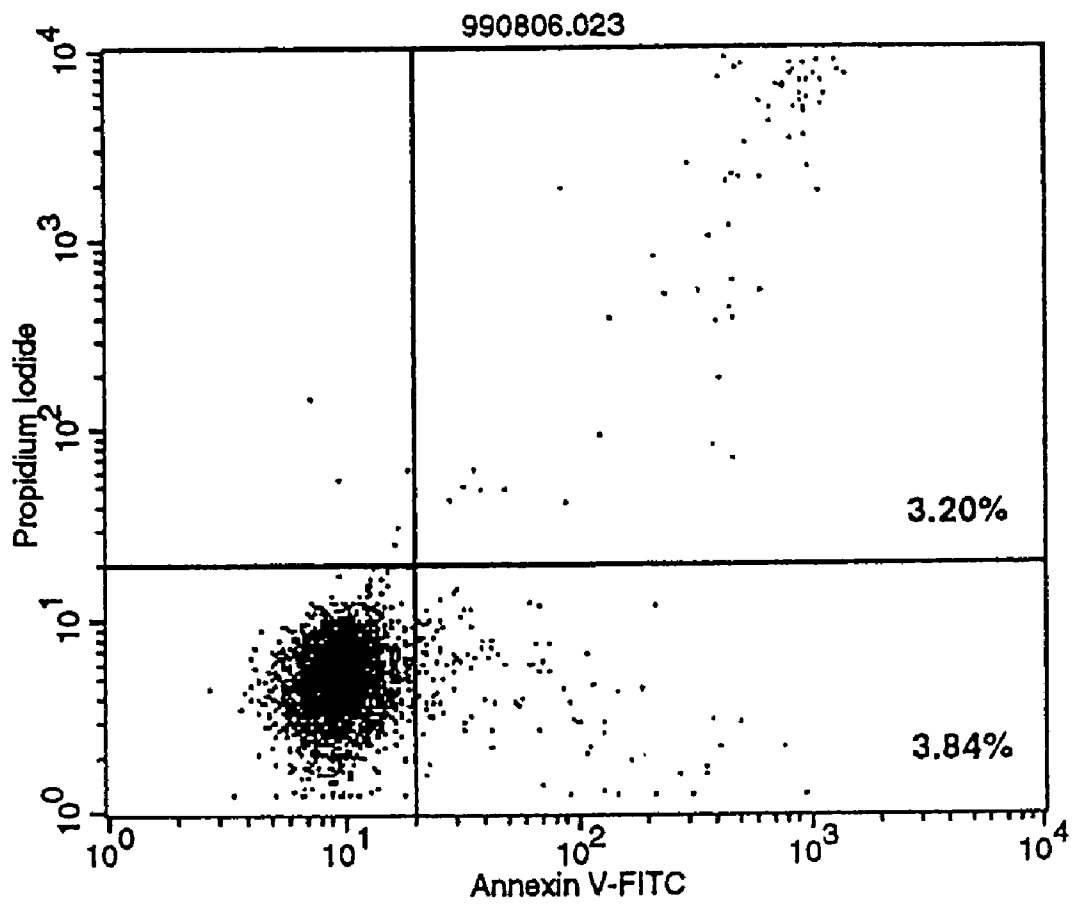


Fig. 30

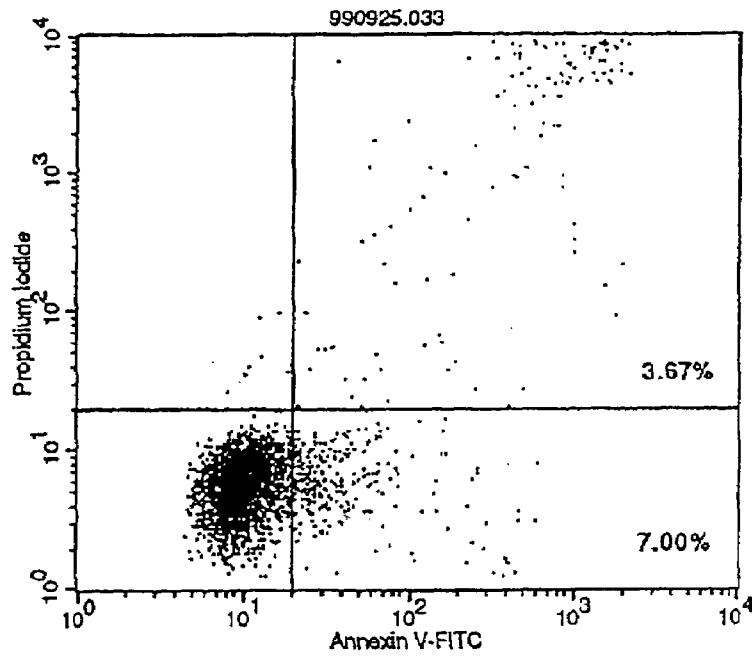


Fig. 31

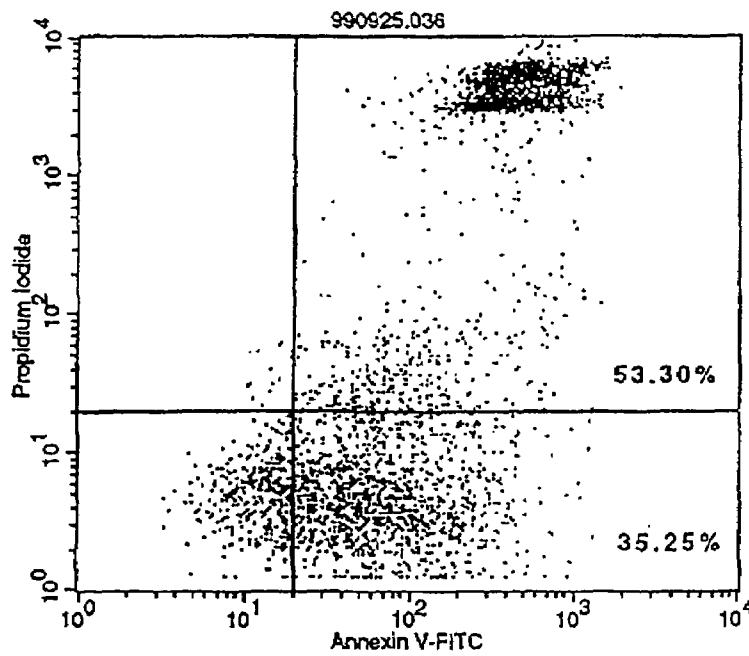


Fig. 32

Effect of MABL-2 (scFv) on serum hlgG in KPMM2 i.v. SCID mice

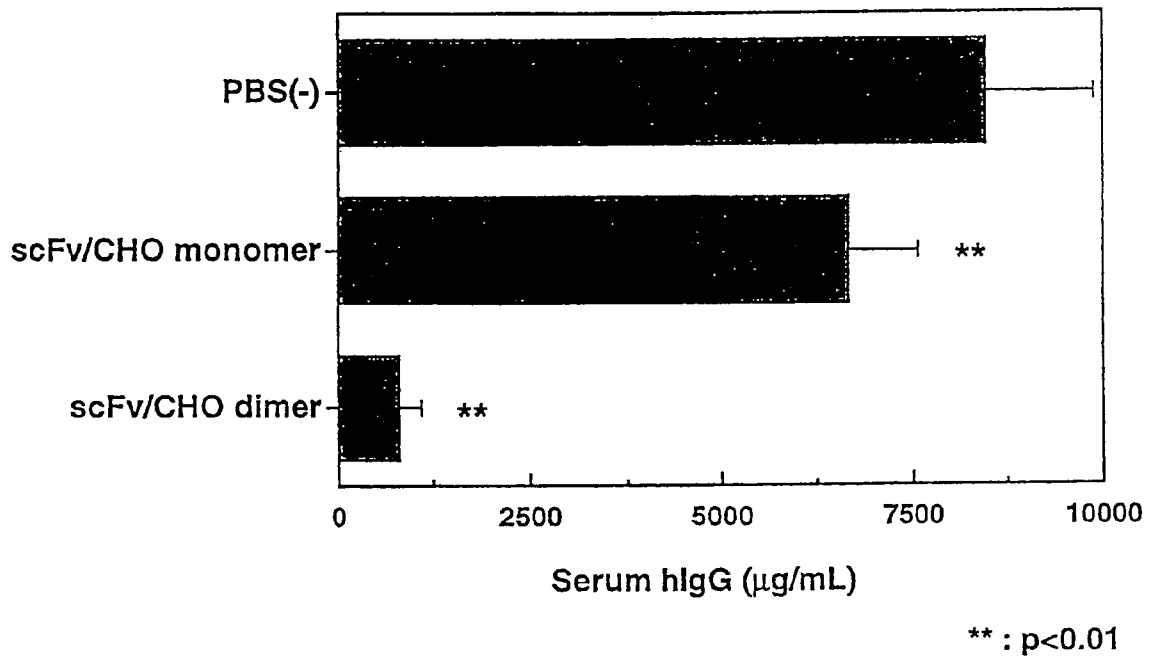
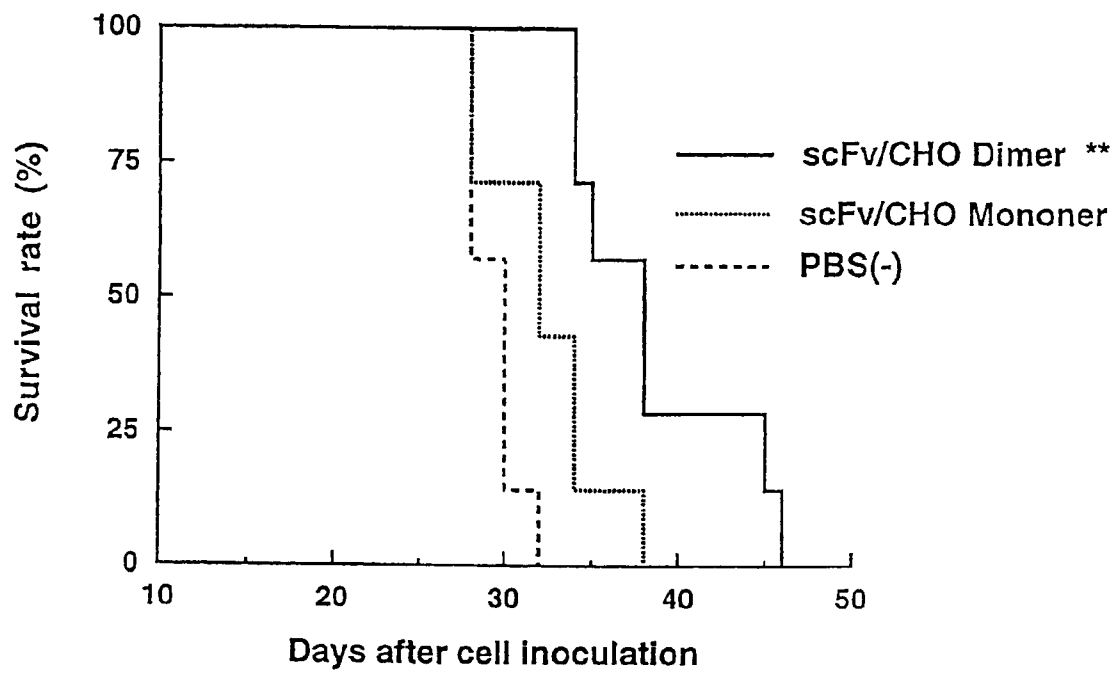


Fig. 33

Effect of MABL-2 (scFv) on survival of KPMM2 i.v. SCID mice



** ; P<0.01 by t-test

Fig. 34

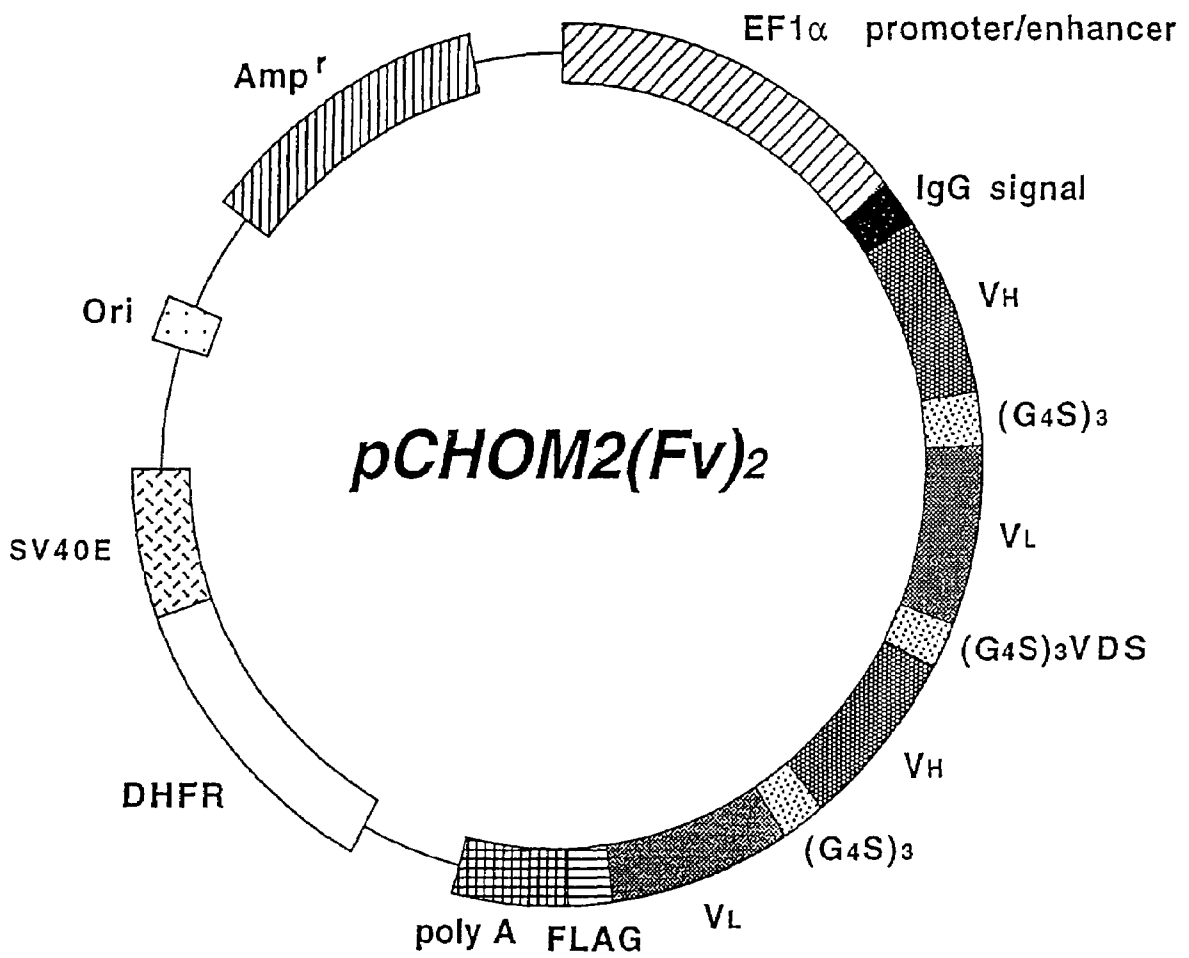


Fig. 35

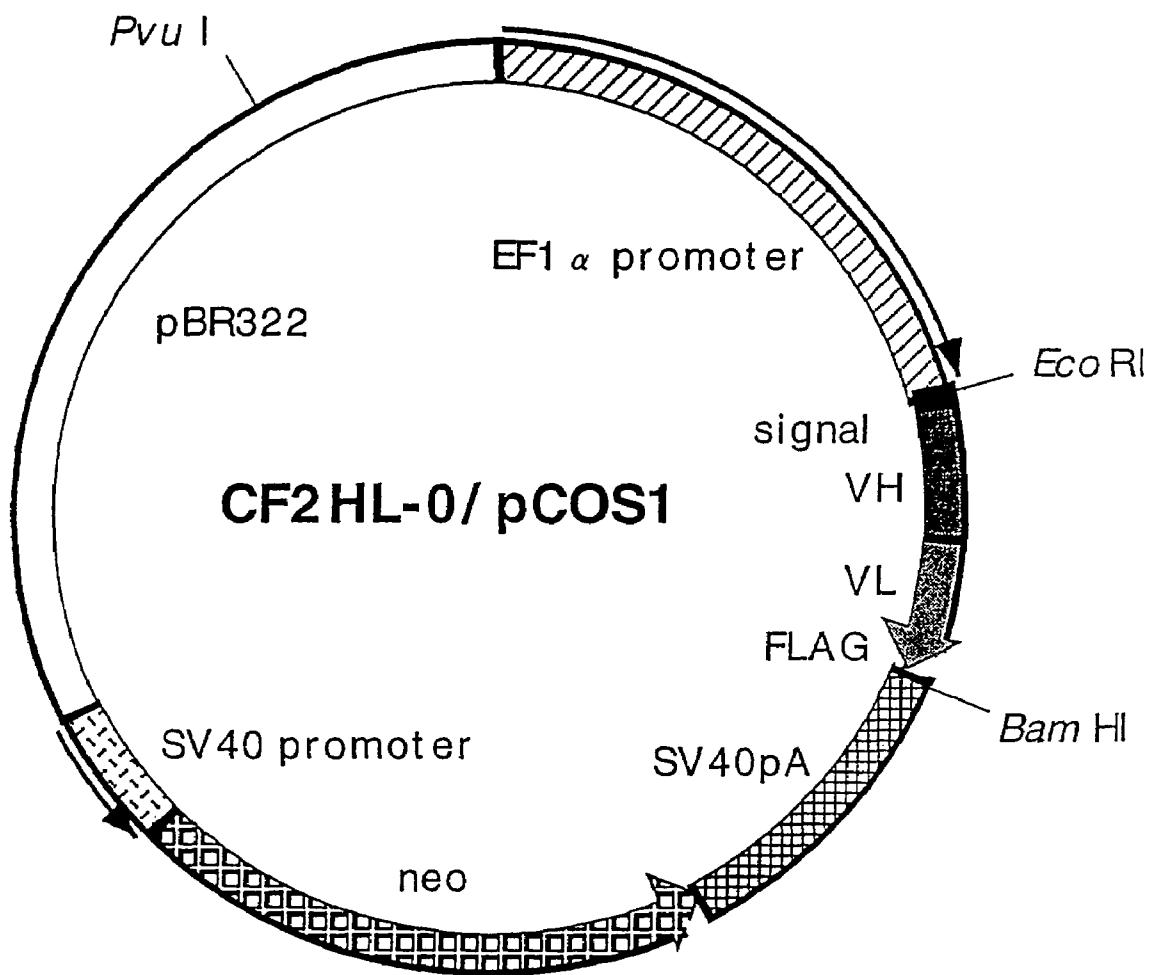
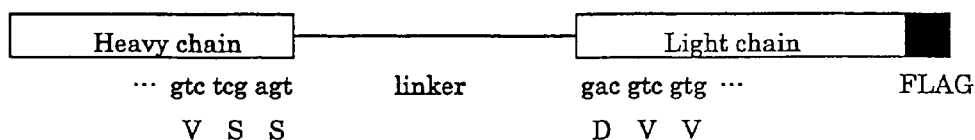


Fig. 36

Base Sequence and Amino Acid Sequence of Linker for HL Type



Plasmid	Number of	
	linker amino acid	linker
CF2HL-0/pCOS1	0	gtc tcg agt V S S
CF2HL-3/pCOS1	3	gtc tcg agt ggt ggt tcc V S S G G S
CF2HL-4/pCOS1	4	gtc tcg agt ggt ggt ggt tcc V S S G G G S
CF2HL-5/pCOS1	5	gtc tcg agt ggt ggt ggt ggt tcc V S S G G G G S
CF2HL-6/pCOS1	6	gtc tcg agt gt ggt ggt ggt ggt tcc V S S G G G G G S
CF2HL-7/pCOS1	7	gtc tcg agt ggt ggt ggt ggt ggt tcc V S S G G G G G G S

Fig. 37

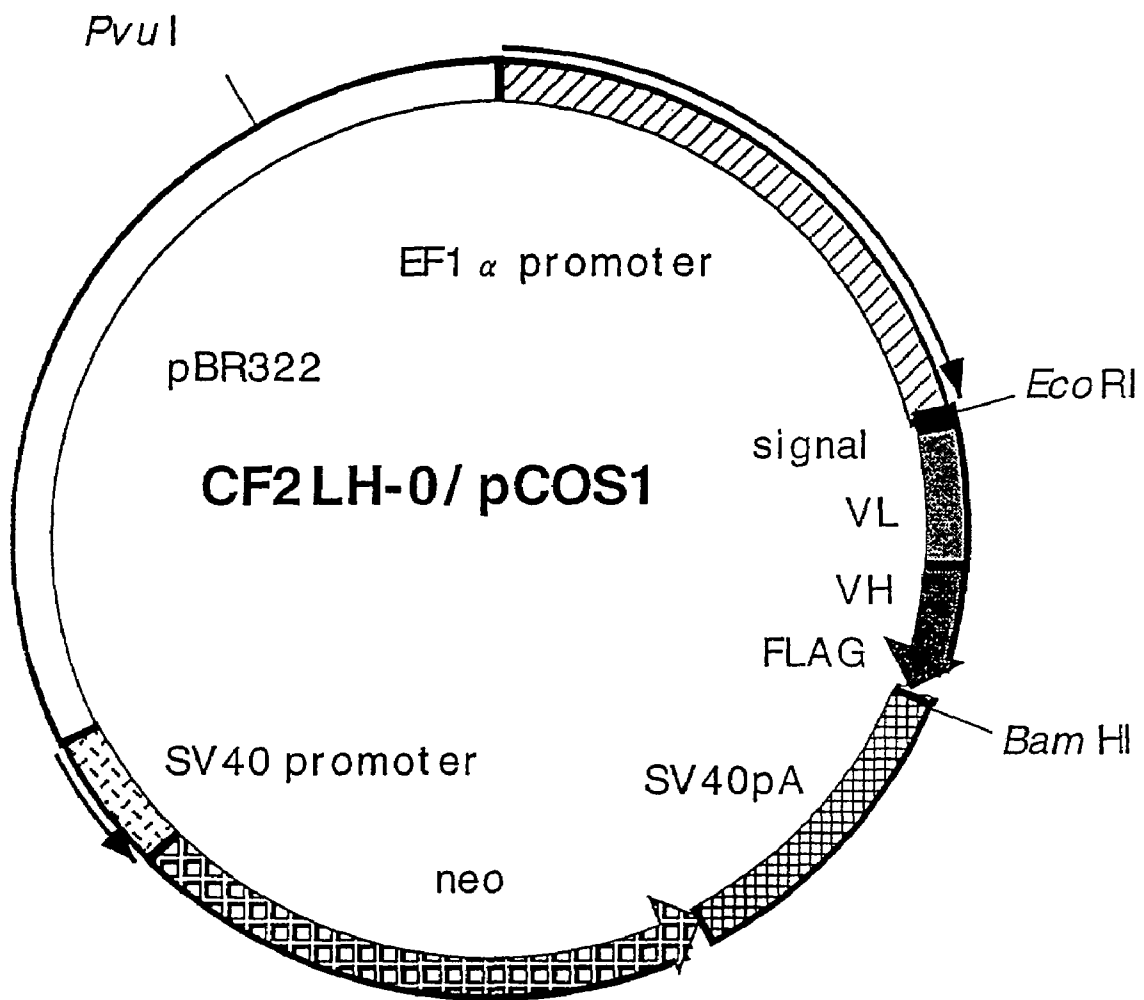
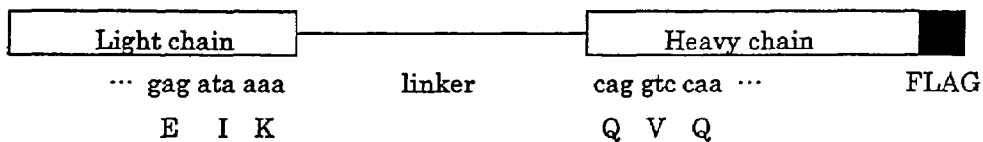


Fig. 38

Base Sequence and Amino Acid Sequence of Linker for HL Type



Plasmid	Number of	
	linker amino acid	linker
CF2LH-0/pCOS1	0	gag ata aaa E I K
CF2LH-3/pCOS1	3	gag ata aaa tcc gga ggc E I K S G G
CF2LH-4/pCOS1	4	gag ata aaa tcc gga ggt ggc E I K S G G G
CF2LH-5/pCOS1	5	gag ata aaa tcc gga ggt ggt ggc E I K S G G G G
CF2LH-6/pCOS1	6	gag ata aaa tcc gga ggt ggt ggt ggc E I K S G G G G G
CF2LH-7/pCOS1	7	gag ata aaa tcc gga ggt ggt ggt ggt ggc E I K S G G G G G G

Fig. 39

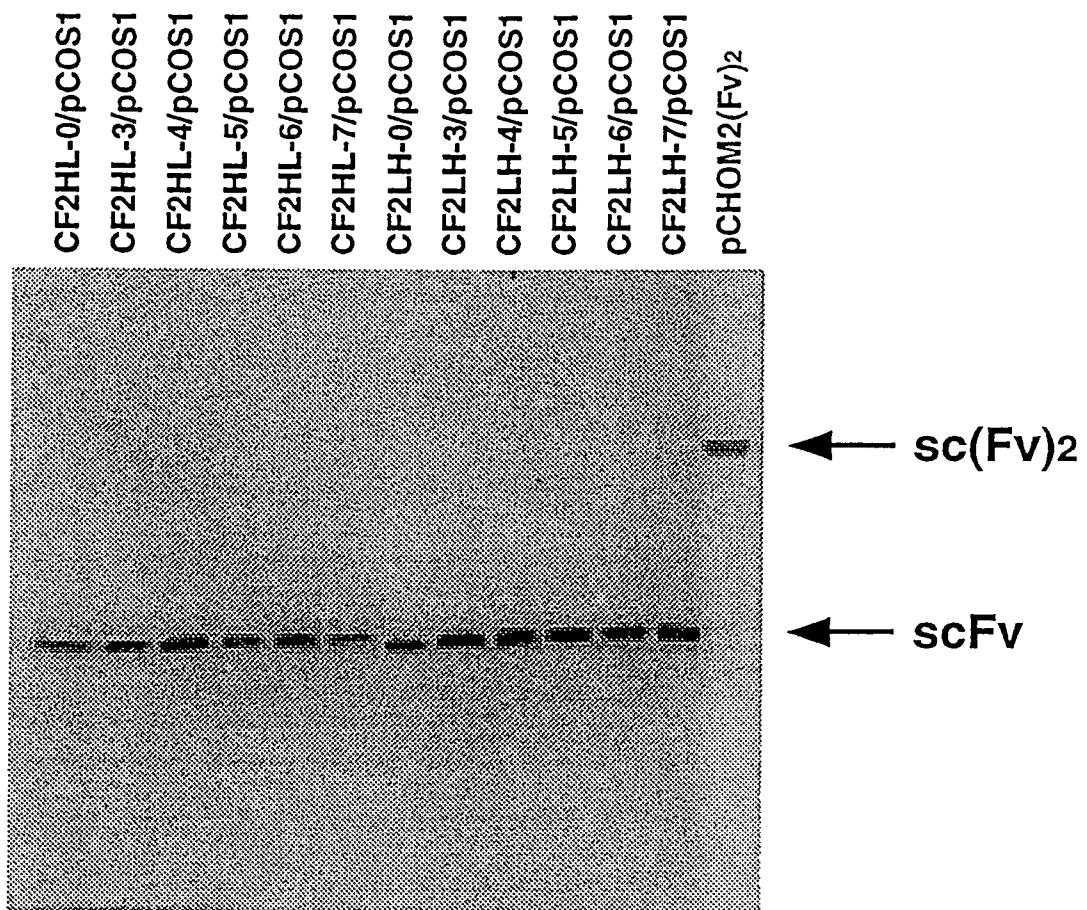


Fig. 40a

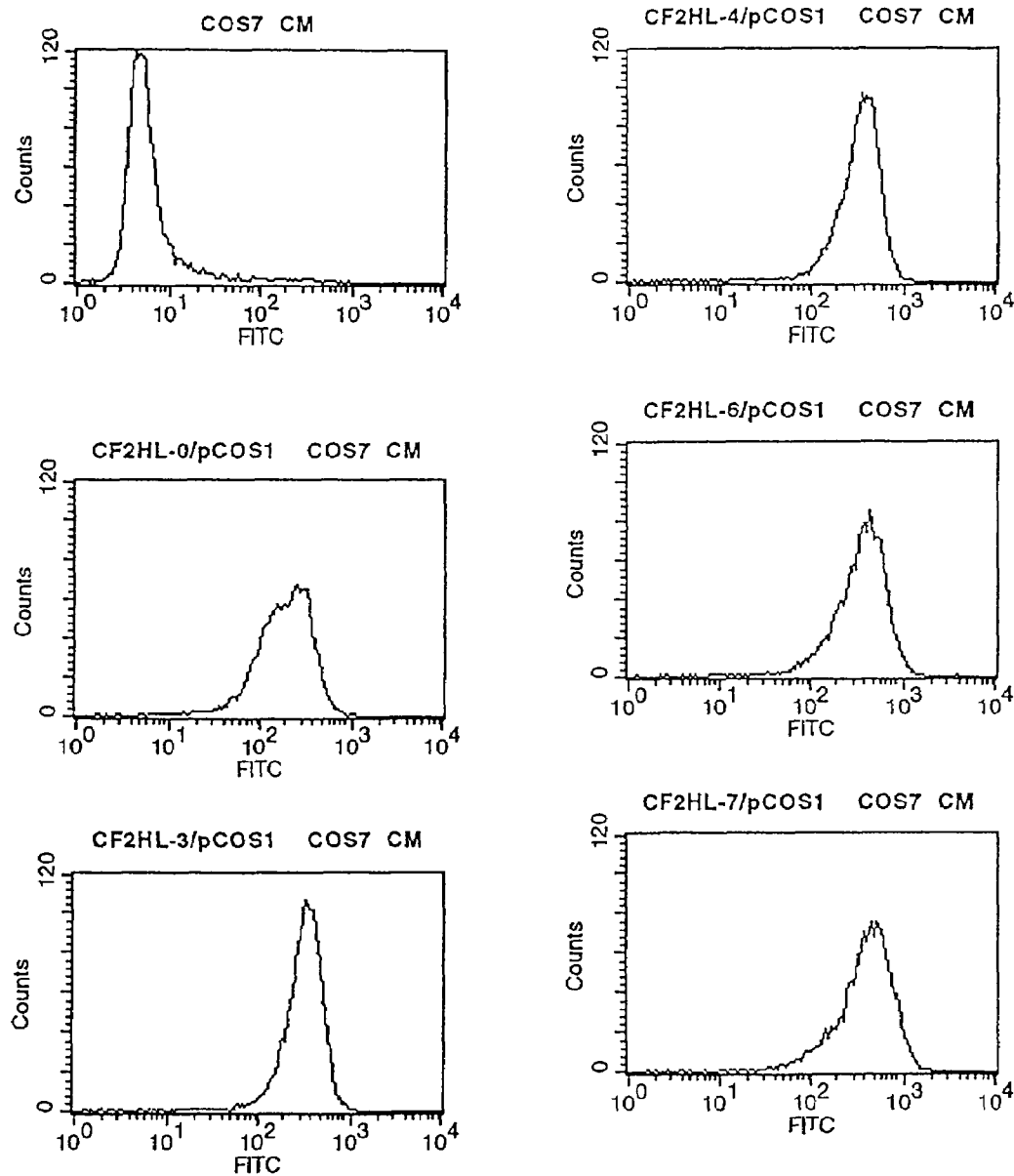


Fig. 40b

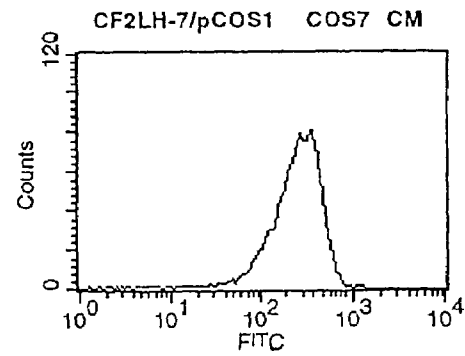
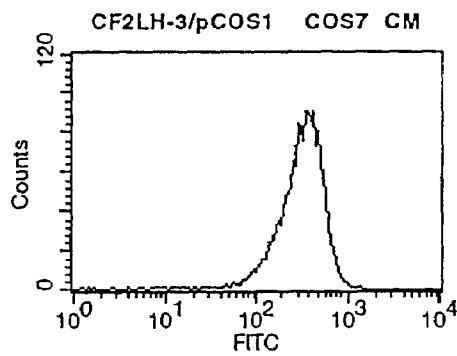
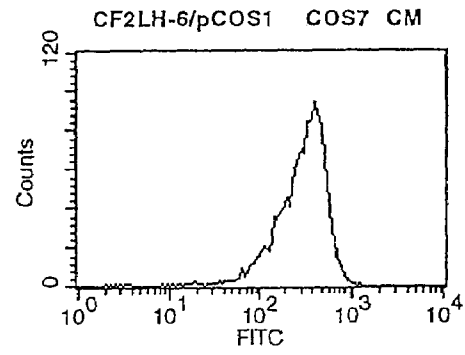
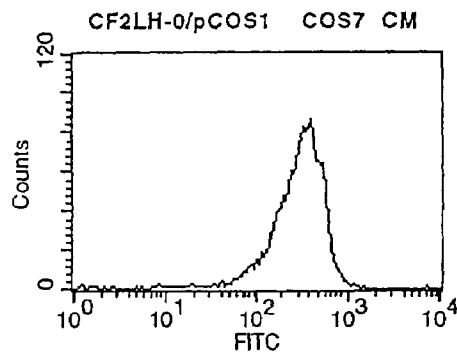
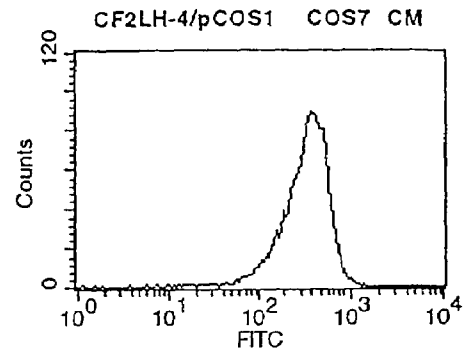
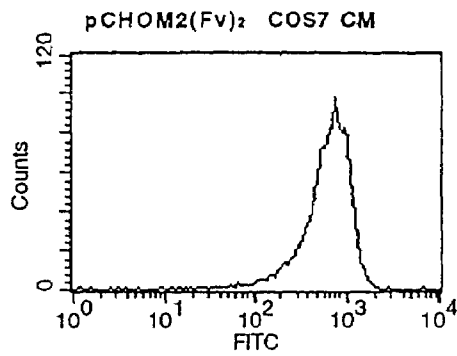


Fig. 41

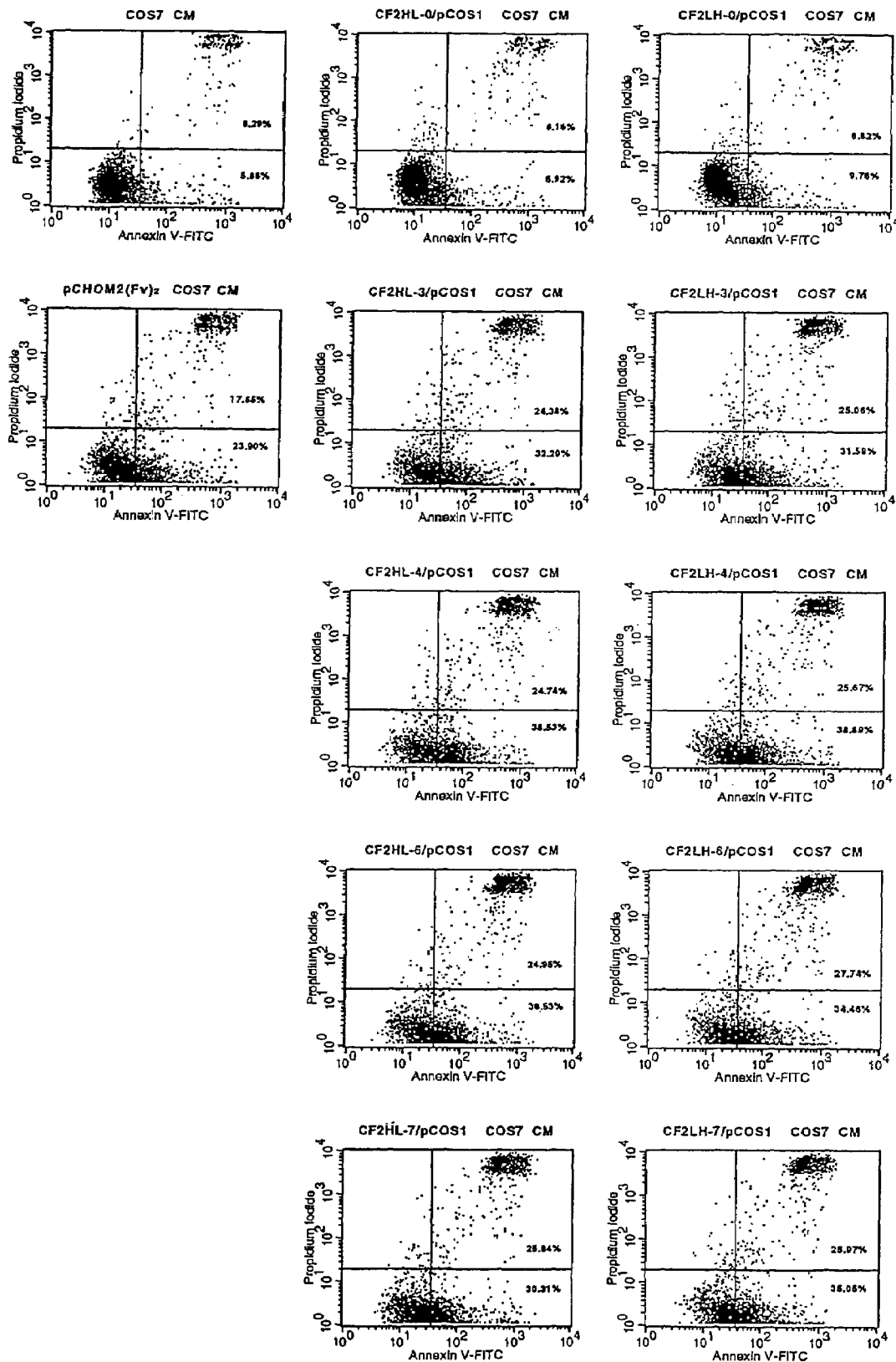


Fig. 42

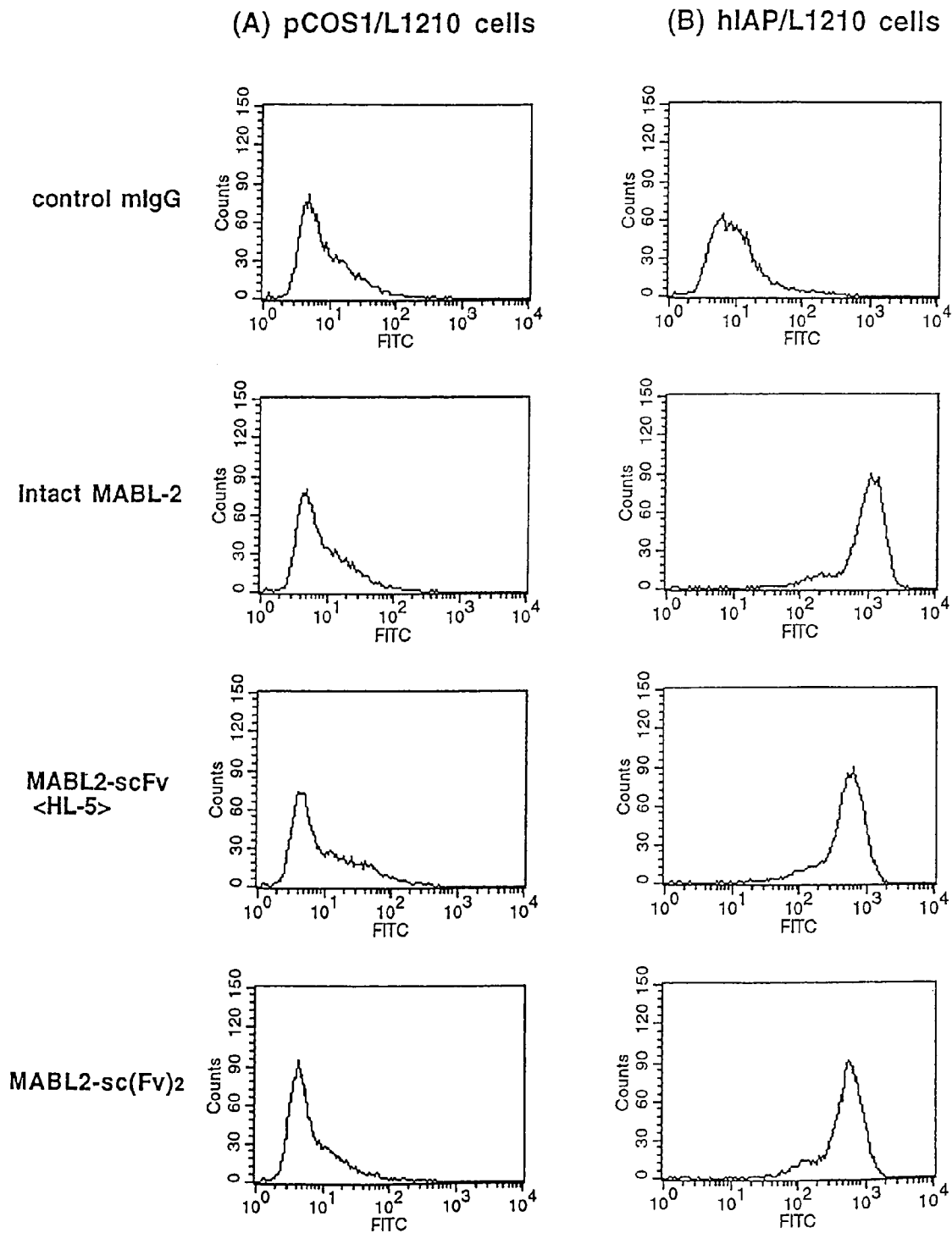


Fig. 43

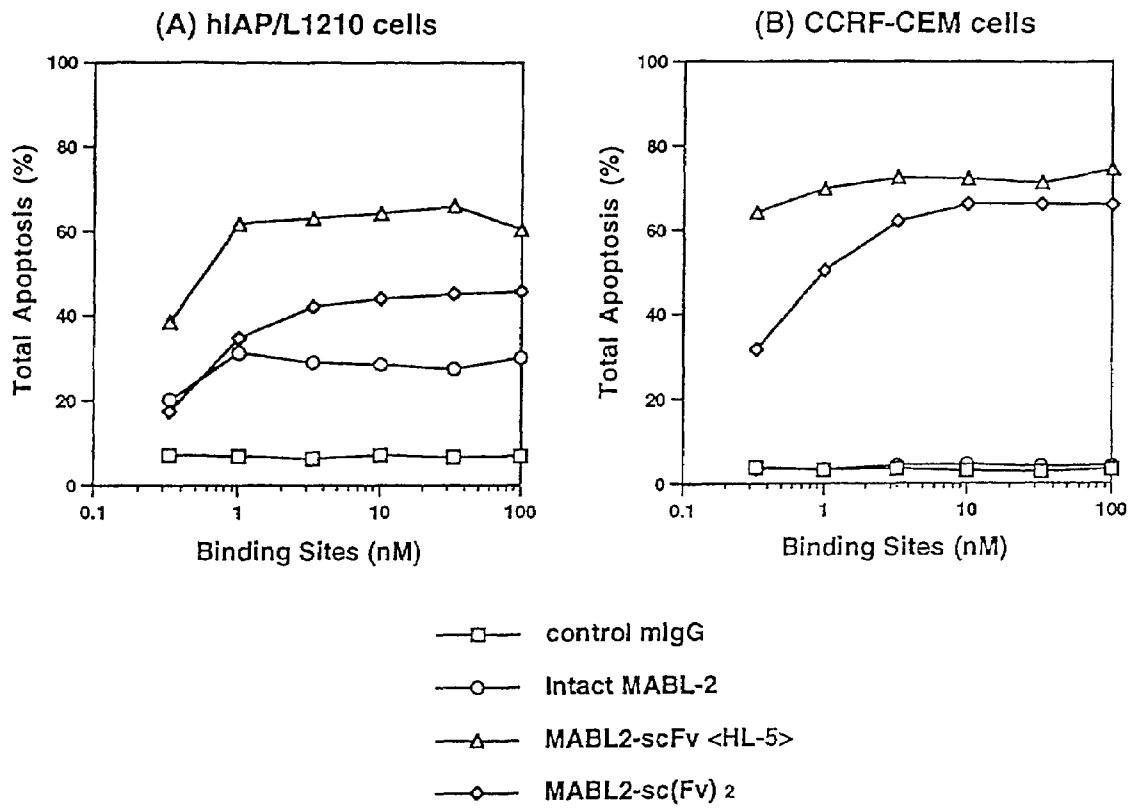


Fig. 44

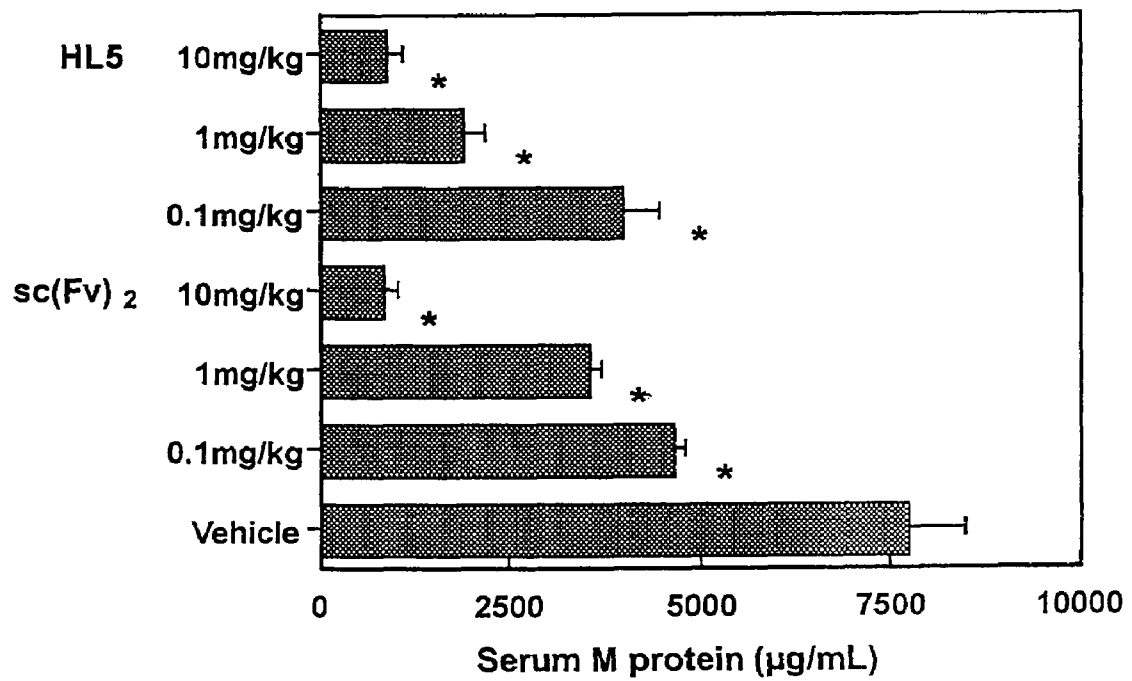


Fig. 45

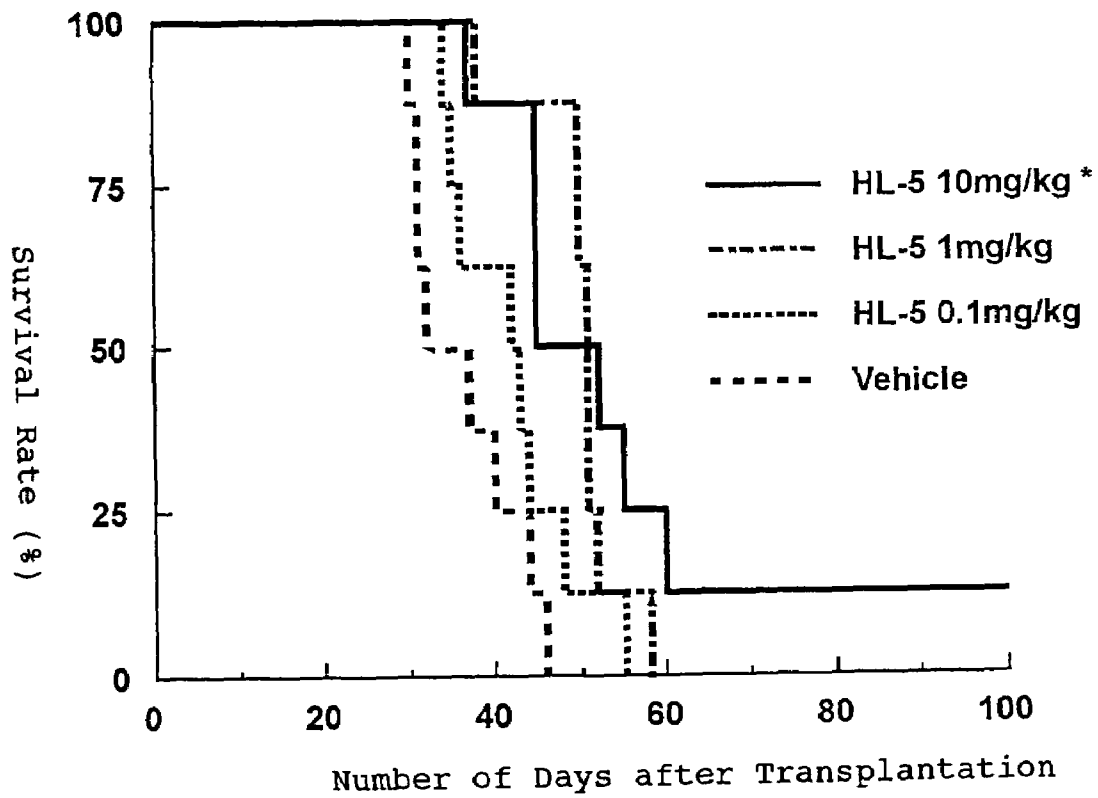
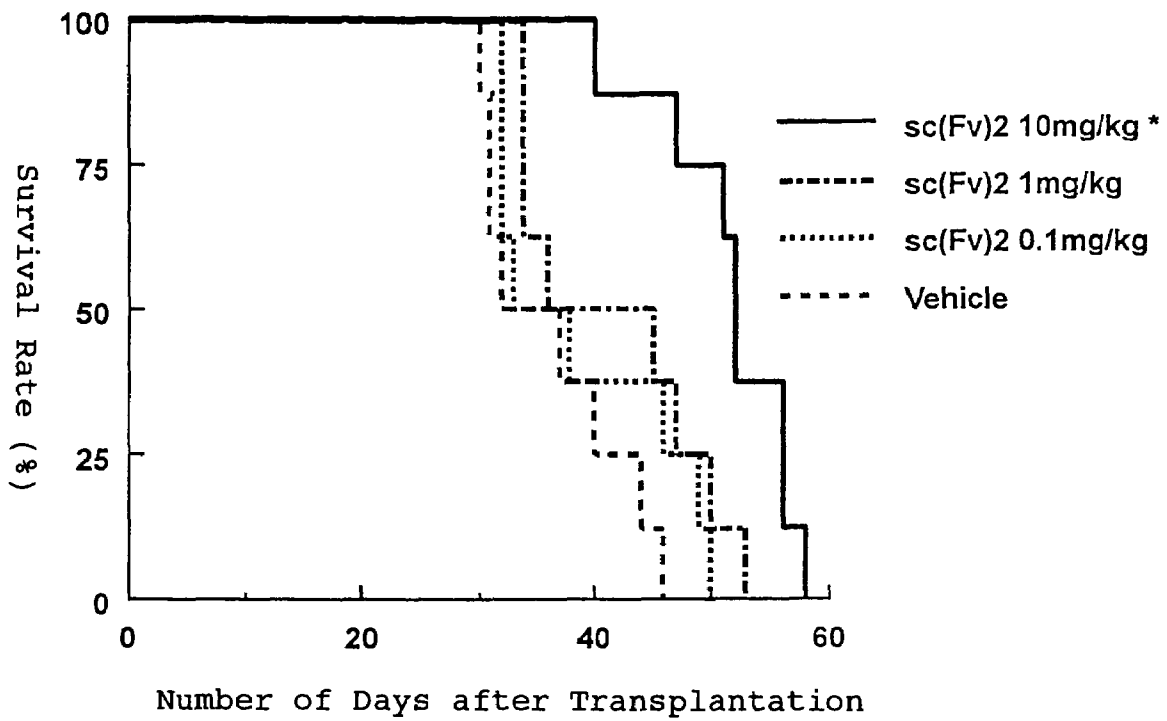


Fig. 46



POLYPEPTIDE INDUCING APOPTOSIS

This application is a continuation-in-part of U.S. application Ser. No. 09/523,095, filed Mar. 10, 2000, now abandoned.

TECHNICAL FIELD

This invention relates to a reconstructed polypeptide with a property of inducing apoptosis of nucleated blood cells having Integrin Associated Protein (IAP) and causing no hemagglutination. More specifically, the present invention relates to the reconstructed polypeptide comprising two or more H chain V regions and two or more L chain V regions of a monoclonal antibody inducing apoptosis of nucleated blood cells having IAP. The reconstructed polypeptides are useful as a therapeutic agent for blood dyscrasia such as leukemia.

BACKGROUND ART

Japanese Patent Application 9-67499 discloses the preparation of a specific monoclonal antibody using a splenic stromal cell line as a sensitizing antigen aiming at developing specific antibodies that can recognize the aforementioned splenic stromal cells and the preparation of novel monoclonal antibodies that recognize mouse Integrin Associated Protein (mouse IAP) as an antigen. JP-Appl. 9-67499 also discloses that the monoclonal antibodies are capable of inducing apoptosis of myeloid cells.

WO99/12973 discloses monoclonal antibodies whose antigen is human Integrin Associated Protein (hereinafter referred to as human IAP; amino acid sequence and nucleotide sequence thereof are described in J. Cell Biol., 123, 485-496, 1993; see also Journal of Cell Science, 108, 3419-3425, 1995) and which are capable of inducing apoptosis of human nucleated blood cells (myeloid cell and lymphocyte) having said human IAP. These monoclonal antibodies are referred to antibody MABL-1 and antibody MABL-2, and hybridomas producing these antibodies are also referred to MABL-1 (FERMBP-6100) and MABL-2 (FERMBP-6101), respectively.

Japanese Patent Application 11-63557 describes the preparation of single-chain Fvs having single chain Fv regions from the monoclonal antibodies whose antigen is human IAP. The single-chain Fvs are capable of inducing apoptosis of nucleated blood cells having human IAP.

The monoclonal antibody recognizing IAP as an antigen induces apoptosis of nucleated blood cells having human IAP, but it also causes hemagglutination in vitro. It indicates that the administration of a large amount of the monoclonal antibody recognizing IAP as an antigen may result in a side effect such as hemagglutination.

DISCLOSURE OF INVENTION

An object of this invention is to provide reconstructed polypeptides with improved property of inducing apoptosis of nucleated blood cells having Integrin Associated Protein (IAP) and with decreased or completely eliminated property of causing hemagglutination. Another object of the present invention is to provide therapeutic agents for blood dyscrasia comprising the substance obtained above which induces apoptosis of nucleated blood cells having Integrin Associated Protein (IAP).

Therefore, the present invention relates to the reconstructed polypeptides which binds to Integrin Associated Pro-

tein (IAP), induces apoptosis of nucleated blood cells having IAP and causes no hemagglutination.

The invention relates also to the reconstructed polypeptides, reshaped antibodies.

5 The reshaped antibody may include any reconstructed polypeptide which comprises an L chain V region and an H chain V region derived from a monoclonal antibody, e.g. antibody MABL-1, antibody MABL-2 or the like inducing apoptosis of nucleated blood cells having IAP, preferably human IAP, which polypeptide induces apoptosis of nucleated blood cells having IAP, preferably human IAP and causes no hemagglutination. Further, the present invention also includes reconstructed polypeptides wherein an amino acid sequence of the V region is partially altered.

15 The present invention also relates to the humanization of the reconstructed polypeptide. The humanized reconstructed polypeptide comprises a humanized L chain V region and/or a humanized H chain V region. Specifically, the humanized polypeptide of the invention consists of the humanized L chain V region which comprises a framework region (FR) derived from an L chain V region of human monoclonal antibody and an CDR derived from an L chain V region of mouse monoclonal antibody and/or the humanized H chain V region which comprises an FR derived from an H chain V region of human monoclonal antibody and a CDR derived from an H chain V region of mouse monoclonal antibody. In this case, the amino acid sequence of FR or CDR may be partially altered, e.g. deleted, replaced or added.

20 Furthermore, the present invention relates to reconstructed polypeptides capable of inducing apoptosis of nucleated blood cells having human IAP, which polypeptides comprise an L chain C region of human antibodies and an L chain V region of the mouse monoclonal antibodies, and/or an H chain C region of human antibodies and an H chain V region of the mouse monoclonal antibodies.

25 The present invention also relates to reconstructed polypeptides inducing apoptosis of nucleated blood cells having human IAP, which polypeptides comprise a CDR derived from a monoclonal antibody of other mammals than mouse such as human, rat, bovine, sheep or the like, which corresponds to the aforementioned mouse CDR, or an L chain V region and an H chain V region which contain the aforementioned CDR. Such CDRs, L chain V regions and H chain V regions may include CDRs derived from a human monoclonal antibody prepared from, for example, a transgenic mouse or the like, and L chain V regions and H chain V regions derived from a human monoclonal antibody containing the aforementioned CDR.

30 The invention also relates to DNAs encoding the various reconstructed polypeptides as aforementioned and genetic engineering techniques for the production of recombinant vectors comprising the DNAs.

35 The invention also relates to host cells transformed with the recombinant vectors. Examples of host cells mammalian cells such as human cells, mouse cells or the like and microorganisms such as *E. coli*, *Bacillus subtilis*, yeast or the like.

40 The invention relates to a process for producing the reconstructed polypeptides, which comprises culturing the above hosts and extracting the reconstructed polypeptides from the culture thereof.

45 The present invention further relates to a process for producing a dimer of the single-chain Fv which comprises culturing host mammalian cells producing the single-chain Fv in a serum-free medium to secrete the single-chain Fv into the medium and isolating the dimer of the single-chain Fv formed in the medium.

The present invention relates to therapeutic agents for blood dyscrasia comprising as an active ingredient the reconstructed polypeptide obtained in the above which induces apoptosis of nucleated blood cells having Integrin Associated Protein (IAP). The therapeutic agents for blood dyscrasia of the invention are useful for the treatment of blood dyscrasia, for example, leukemia such as acute myeloid leukemia, chronic myelogenous leukemia, acute lymphoblastic leukemia, chronic lymphoblastic leukemia, adult T-cell leukemia, multiple myeloma, mixed leukemia and hairy cell leukemia, malignant lymphoma (Hodgkin's disease, non-Hodgkin's lymphoma), aplastic anemia, myelodysplasia syndrome and polycythemia vera.

The reconstructed polypeptides of the present invention preferably comprise two H chain V regions and two L chain V regions derived from the monoclonal antibodies. The structure of the reconstructed polypeptides may be a dimer of single-chain Fv comprising one H chain V region and one L chain V region or a polypeptide comprising two H chain V regions and two L chain V regions. In the reconstructed polypeptides of the invention, the H chain V region and the L chain V region are preferably linked through a peptide linker which consists of one or more amino acids. The resulting reconstructed polypeptides contain variable regions of the parent antibodies and retain the complementarity determining region (CDR) thereof, and therefore bind to the antigen with the same specificity as that of the parent monoclonal antibodies.

H Chain V Region

In the present invention, the H chain V region derived from the monoclonal antibody can be the H chain V region of the monoclonal antibody inducing apoptosis of nucleated blood cells having IAP or the H chain V region whose amino acid sequence is partially modified, preferably the H chain V region of the monoclonal antibody recognizing human IAP and inducing apoptosis of nucleated blood cells having IAP or the H chain V region whose amino acid sequence is partially modified. Preferable is the H chain V region derived from antibody MABL-1 or antibody MABL-2, or the H chain V region wherein the amino acid sequence of the H chain V region is partially modified. More preferable is humanized H chain V region comprising FR from an H chain V region of human monoclonal antibody and CDR from the H chain V region of mouse monoclonal antibody. The H chain V region further can be an H chain V region derived from a human monoclonal antibody corresponding to the aforementioned H chain V region of mouse monoclonal antibody, which can be produced by recombination technique. The H chain V region of the invention may be a fragment of aforementioned H chain V region, which fragment preserves the antigen binding capacity.

L Chain V Region

The L chain V region of the present invention can be L chain V region of the monoclonal antibody inducing apoptosis of nucleated blood cells having IAP or the L chain V region wherein the amino acid sequences of the L chain V region is partially modified, preferably the L chain V region of the monoclonal antibody recognizing human IAP and inducing apoptosis of nucleated blood cells having IAP or the L chain V region whose amino acid sequences is partially modified. Preferable is L chain V region derived from antibody MABL-1 or antibody MABL-2, or its L chain V region whose amino acid sequence is partially modified. More preferable is humanized L chain V region comprising FR from L chain V region of human monoclonal antibody and CDR from the L chain V region of mouse monoclonal antibody. The L chain V

regions further can be an L chain V region derived from human monoclonal antibody corresponding to the aforementioned L chain V region of mouse monoclonal antibody, which can be produced by recombination technique. The L chain V regions of the invention may be fragments of L chain V region, which fragments preserve the antigen binding capacity.

Complementarity Determining Region (CDR)

Each V region of L chain and H chain forms an antigen-binding site. The variable region of the L and H chains is composed of comparatively conserved four common framework regions linked to three hypervariable regions or complementarity determining regions (CDR) (Kabat, E. A. et al., "Sequences of Protein of Immunological Interest", US Dept. Health and Human Services, 1983).

Major portions in the four framework regions (FRs) form β -sheet structures and thus three CDRs form a loop. CDRs may form a part of the β -sheet structure in certain cases. The three CDRs are held sterically close position to each other by FR, which contributes to the formation of the antigen-binding site together with three CDRs.

These CDRs can be identified by comparing the amino acid sequence of V region of the obtained antibody with known amino acid sequences of V regions of known antibodies according to the empirical rule in Kabat, E. A. et al., "Sequences of Protein of Immunological Interest".

Single-Chain Fv

A single-chain Fv is a polypeptide monomer comprising an H chain V region and an L chain V region linked each other which are derived from monoclonal antibodies. The resulting single-chain Fvs contain variable regions of the parent monoclonal antibodies and preserve the complementarity determining region thereof, and therefore the single-chain Fvs bind to the antigen by the same specificity as that of the parent monoclonal antibodies (JP-Appl. 11-63557). A part of the variable region and/or CDR of the single-chain Fv of the invention or a part of the amino acid sequence thereof may be partially altered, for example deleted, replaced or added. The H chain V region and L chain V region composing the single-chain Fv of the invention are mentioned before and may be linked directly or through a linker, preferably a peptide linker. The constitution of the single-chain Fv may be [H chain V region]-[L chain V region] or [L chain V region]-[H chain V region]. In the present invention, the single-chain Fv can form a dimer, trimer or which can be tetramer included in the reconstructed polypeptide of the invention.

Single-Chain Reconstructed Polypeptide

The single-chain reconstructed polypeptides of the present invention comprising two or more H chain V regions and two or more L chain V regions comprise two or more H chain V regions and L chain V regions as mentioned above. Each region of the peptide should be arranged such that the reconstructed single chain polypeptide forms a specific steric structure, concretely mimicking a steric structure formed by the dimer of single-chain Fv. For instance, the V regions are arranged in the order of the following manner:

[H chain V region]-[L chain V region]-[H chain V region]-[L chain V region]; or

[L chain V region]-[H chain V region]-[L chain V region]-[H chain V region],

wherein these regions are connected through a peptide linker, respectively.

Linker

In this invention, the linkers for the connection between the H chain V region and the L chain V region may be any peptide linker which can be introduced by the genetic engineering procedure or any linker chemically synthesized. For instance, linkers disclosed in literatures, e.g. Protein Engineering, 9(3), 299-305, 1996 may be used in the invention. Examples of the peptide linkers may include, for example;

Ser
 Gly-Ser
 Gly-Gly-Ser
 Ser-Gly-Gly
 Gly-Gly-Gly-Ser (SEQ ID NO: 80)
 Ser-Gly-Gly-Gly (SEQ ID NO: 81)
 Gly-Gly-Gly-Gly-Ser (SEQ ID NO: 82)
 Ser-Gly-Gly-Gly-Gly (SEQ ID NO: 83)
 Gly-Gly-Gly-Gly-Gly-Ser (SEQ ID NO: 84)
 Ser-Gly-Gly-Gly-Gly-Gly (SEQ ID NO: 85)
 Gly-Gly-Gly-Gly-Gly-Gly-Ser (SEQ ID NO: 86)
 Ser-Gly-Gly-Gly-Gly-Gly-Gly (SEQ ID NO: 87)
 (Gly-Gly-Gly-Gly-Ser)_n (SEQ ID NO: 88) and
 (Ser-Gly-Gly-Gly-Gly)_n (SEQ ID NO: 89)

wherein n is an integer not less than one. Length of the peptide linker is in the range of 1 to 15 amino acids, preferably 2 to 12 amino acids, more preferably 3 to 10 amino acids. Procedures for introducing these linkers are mentioned in Explanation of DNA encoding the reconstructed polypeptide or the invention.

The chemically synthesized linkers, i.e. the chemical crosslinking agents, according to the invention can be any linkers conventionally employed for the linkage of peptides. Examples of the linkers may include N-hydroxy succinimide (NHS), disuccinimidyl suberate (DSS), bis(sulfosuccinimidyl)suberate (BS³), dithiobis(succinimidyl propionate) (DSP), dithiobis(sulfosuccinimidyl propionate) (DTSSP), ethylene glycolbis(succinimidyl succinate) (EGS), ethylene glycolbis(sulfosuccinimidyl succinate) (sulfo-EGS), disuccinimidyl tartrate (DST), disulfosuccinimidyl tartrate (sulfo-DST), bis[2-(succinimido oxycarbonyloxy)ethyl]sulfone (BSOCOES), bis[2-(sulfosuccinimido oxycarbonyloxy)ethyl]sulfone (sulfo-BSOCOES) or the like. These are commercially available.

To form a dimer of the single-chain Fv it is preferable to select a linker suitable to dimerize in the solution such as culture medium more than 20%, preferably more than 50%, more preferably more than 80%, most preferably more than 90% of the single-chain Fv produced in the host cells. Specifically, preferable is a linker composed of 2 to 12 amino acids, preferably 3 to 10 amino acids or other linkers corresponding thereto.

Preparation of Reconstructed Polypeptides

The reconstructed polypeptide binding to cells with human IAP are obtainable by connecting an H chain V region and an L chain V region derived from monoclonal antibodies against human IAP through the aforementioned linker. Examples of

the single-chain Fvs are MABL1-scFv comprising the H chain V region and the L chain V region derived from the antibody MABL-1, and MABL2-scFv comprising the H chain V region and the L chain V region derived from the antibody MABL-2.

For the preparation of the reconstructed polypeptide, a signal peptide may be attached to N-terminal of the polypeptide where the polypeptide is desired to be a secretory peptide. A well-known amino acid sequence useful for the purification of polypeptide such as the FLAG sequence may be attached for the efficient purification of the polypeptide. The polypeptide can be efficiently purified with anti-FLAG antibody.

For the preparation of the reconstructed polypeptide of the invention, it is necessary to obtain a DNA encoding the reconstructed polypeptide, i.e. a DNA encoding the single-chain Fv or a DNA encoding the reconstructed polypeptide monomer. These DNAs are obtainable from the DNAs encoding the H chain V region and the L chain V region of MABL1-scFv and/or MABL2-scFv. They are also obtainable by amplifying a DNA encoding desired amino acid sequence within the aforementioned sequence by PCR using the DNA as a template and a pair of primers corresponding to both ends thereof.

In the case where each V region having partially modified amino acid sequence is desired, the V regions in which one or some amino acids are modified, i.e. deleted, replaced or added can be obtained by a procedure known in the art using PCR. A part of the amino acid sequence in the V region is preferably modified by the PCR known in the art in order to prepare the reconstructed polypeptide which is sufficiently active against the specific antigen.

For the determination of primers for the PCR amplification, it is necessary to decide the type of the H chain and L chain of the antibody MABL-1 and/or the antibody MABL-2. It has been reported, however, that the antibody MABL-1 has κ type L chains and γ 1 type H chains and the antibody MABL-2 has κ type L chains and γ 2a type H chains (JP-App. 11-63557). For the PCR amplification of the DNA encoding the H chain and L chain of the antibody MABL-1 and/or the antibody MABL-2, primers described in Jones, S. T. et al., Bio/Technology, 9, 88-89, 1991 may be employed.

For the amplification of the L chain V regions of the antibody MABL-1 and the antibody MABL-2 using the polymerase chain reaction (PCR), 5'-end and 3'-end oligonucleotide primers are decided as aforementioned. In the same manner, 5'-end and 3'-end oligonucleotide primers are decided for the amplification of the H chain V regions of the antibody MABL-1 and the antibody MABL-2.

In embodiments of the invention, the 5'-end primers which contain a sequence "GANTC" providing the restriction enzyme Hinf I digestion site at the neighborhood of 5'-terminal thereof are used and the 3'-end primers which contain a nucleotide sequence "CCCGGG" providing the XmaI digestion site at the neighborhood of 5'-terminal thereof are used. Other restriction enzyme digestion sites may be used instead of these sites as long as they are used for subcloning a desired DNA fragment into a cloning vector.

Specifically designed PCR primers are employed to provide suitable nucleotide sequences at 5'-end and 3'-end of the cDNAs encoding the V regions of the antibodies MABL-1 and MABL-2 so that the cDNAs are readily inserted into an expression vector and appropriately function in the expression vector (e.g. this invention devises to increase transcription efficiency by inserting Kozak sequence). The V regions of the antibodies MABL-1 and MABL-2 obtained by amplifying by PCR using these primers are inserted into HEF expression vector containing the desired human C region (see WO92/19759). The cloned DNAs can be sequenced by using

any conventional process which comprises, for example, inserting the DNAs into a suitable vector and then sequencing using the automatic DNA sequencer (Applied Biosystems).

A linker such as a peptide linker can be introduced into the reconstructed polypeptide of the invention in the following manner. Primers which have partially complementary sequence with the primers for the H chain V regions and the L chain V regions as described above and which code for the N-terminal or the C-terminal of the linker are designed. Then, the PCR procedure can be carried out using these primers to prepare a DNA encoding the peptide linker having desired amino acid sequence and length. The DNAs encoding the H chain V region and the L chain V region can be connected through the resulting DNA to produce the DNA encoding the reconstructed polypeptide of the invention which has the desired peptide linker. Once the DNA encoding one of the reconstructed polypeptides is prepared, the DNAs encoding the reconstructed polypeptides with or without the desired peptide linker can readily be produced by designing various primers for the linker and then carrying out the PCR using the primers and the aforementioned DNA as a template.

Each V region of the reconstructed polypeptide of the present invention can be humanized by using conventional techniques (e.g. Sato, K. et al., *Cancer Res.*, 53, 851-856 (1993)). Once a DNA encoding a humanized Fv is prepared, a humanized single-chain Fv, a fragment of the humanized single-chain Fv, a humanized monoclonal antibody and a fragment of the humanized monoclonal antibody can readily be produced according to conventional methods. Preferably, amino acid sequences of the V regions thereof may be partially modified, if necessary.

Furthermore, a DNA derived from other mammalian origin, for example a DNA of human, can be produced in the same manner as used to produce DNA encoding the H chain V region and the L chain V region derived from mouse mentioned in the above. The resulting DNA can be used to prepare an H chain V region and an L chain V region of other mammal, especially human origin, a single-chain Fv derived from human and a fragment thereof, and a monoclonal antibody of human origin and a fragment thereof.

As mentioned above, when the aimed DNAs encoding the V regions of the reconstructed polypeptides and the V regions the reconstructed humanized polypeptides are prepared, the expression vectors containing them and hosts transformed with the vectors can be obtained according to conventional methods. Further, the hosts can be cultured according to a conventional method to produce the reconstructed single-chain Fv, the reconstructed humanized single-chain Fv, the humanized monoclonal antibodies and fragments thereof. They can be isolated from cells or a medium and can be purified into a homogeneous mass. For this purpose any isolation and purification methods conventionally used for proteins, e.g. chromatography, ultra-filtration, salting-out and dialysis, may be employed in combination, if necessary, without limitation thereto.

When the reconstructed single-chain Fv of the present invention is produced by culturing an animal cell such as COS7 cells or CHO cells, preferably CHO cells, in a serum-free medium, the reconstructed single-chain Fv is efficiently dimerized in the medium. The dimer of the single-chain Fv as formed above can be isolated stably and efficiently and preserved for a long period in the dimer form. The serum-free medium employed in the invention may be any medium conventionally used for the production of a recombinant protein without limit thereto.

For the production of the reconstructed polypeptides binding to cells with human IAP of the present invention, any

expression systems can be employed, for example, eukaryotic cells such as animal cells, e.g., established mammalian cell lines, filamentous fungi and yeast, and prokaryotic cells such as bacterial cells e.g., *E. coli*. Preferably, the reconstructed polypeptides of the invention are expressed in mammalian cells, for example COS7 cells or CHO cells.

In these cases, conventional promoters useful for the expression in mammalian cells can be used. Preferably, human cytomegalovirus (HCMV) immediate early promoter is used. Expression vectors containing the HCMV promoter include HCMV-VH-HC γ 1, HCMV-VL-HCK and the like which are derived from pSV2neo (WO92/19759).

Additionally, other promoters for gene expression in mammal cell which may be used in the invention include virus promoters derived from retrovirus, polyoma virus, adenovirus and simian virus 40 (SV40) and promoters derived from mammal such as human polypeptide-chain elongation factor-1 α (HEF-1 α). SV40 promoter can easily be used according to the method of Mulligan, R. C., et al. (*Nature* 277, 108-114 (1979)) and HEF-1 α promoter can also be used according to the methods of Mizushima, S. et al. (*Nucleic Acids Research*, 18, 5322 (1990)).

Replication origin (ori) which can be used in the invention includes ori derived from SV40, polyoma virus, adenovirus, bovine papilloma virus (BPV) and the like. For the purpose of the amplification of gene copy number in the host cell system and the like, an expression vector may contain, as a selection marker, phosphotransferase APH (3') II or I (neo) gene, thymidine kinase (TK) gene, *E. coli* xanthine-guanine phosphoribosyl transferase (Ecogpt) gene or dihydrofolate reductase (DHFR) gene.

The antigen-binding activity of the reconstructed polypeptide as prepared above can be evaluated using the binding-inhibitory ability of the mouse antibodies, MABL-1 and MABL-2, to human IAP as an index. Concretely, the activity is evaluated in terms of the absence or presence of concentration-dependent inhibition of the binding of the mouse antibody MABL-2 to human IAP antigen as an index.

More in detail, animal cells transformed with an expression vector containing a DNA encoding the reconstructed polypeptide of the invention, e.g., COS7 cells or CHO cells, are cultured. The cultured cells and/or the supernatant of the medium or the reconstructed polypeptide purified from them are used to determine the binding to antigen. As a control, a supernatant of the cultural medium is used in which cells transformed only with the expression vector were cultured. A test sample of the reconstructed polypeptide of the invention or the supernatant of the control is added to mouse leukemia cell line, L1210 cells, expressing human Integrin Associated Protein (IAP) and then an assay such as the flow cytometry is carried out to evaluate the antigen-binding activity.

The apoptosis-inducing effect in vitro is evaluated in the following manner: A test sample of the above reconstructed polypeptide is added to the cells into which the human IAP gene has been introduced and is evaluated on its inducibility of human IAP-specific cell death in the cells.

The apoptosis-inducing effect in vivo is evaluated in the following manner: A mouse model of human myeloma is prepared. To the mice is intravenously administered the monoclonal antibody or the reconstructed polypeptide of the invention, which induces apoptosis of nucleated blood cells having IAP. To mice of a control group is administered PBS alone. The induction of apoptosis is evaluated in terms of antitumor effect based on the change of human IgG content in serum of the mice and their survival time.

Hemagglutination effect is tested in the following manner: A suspension of erythrocytes is prepared from blood of

healthy donors. Test samples of different concentrations are added to the suspension, which are then incubated to determine the hemagglutination.

Reconstructed polypeptides of the invention, which comprises two or more H chain V regions and two or more L chain V regions, may be a dimer, trimer or tetramer of the single-chain Fv comprising one H chain V region and one L chain V region, or a polypeptide in which two or more H chain V regions and two or more L chain V regions are connected. It is considered that owing to such construction the peptide mimics three dimensional structure of the antigen binding site of the parent monoclonal antibody and therefore retains an excellent antigen-binding property.

The polypeptide of the invention has a superior mobility to tissues or tumors over whole IgG and a remarkably reduced or no side effect of hemagglutination. Therefore, it is expected that the peptide of the invention can be used as a therapeutic agent for blood dyscrasia, for example, leukemia such as acute myeloid leukemia, chronic myelogenous leukemia, acute lymphoblastic leukemia, chronic lymphoblastic leukemia, adult T-cell leukemia, multiple myeloma, mixed leukemia and hairy cell leukemia, malignant lymphoma (Hodgkin's disease, non-Hodgkin's lymphoma), hypoplastic anemia, osteomyelodysplasia and polycythemia vera. It is further expected that the peptide of the invention can be used as a contrast agent by RI-labeling. The effect of the peptide can be enhanced by attaching to a RI-compound or a toxin.

BEST MODE FOR WORKING THE INVENTION

The present invention will concretely be illustrated in reference to the following examples, which in no way limit the scope of the invention.

For illustrating the production process of the reconstructed polypeptides of the invention, examples of producing single-chain Fvs are shown below. Mouse antibodies against human IAP, MABL-1 and MABL-2 were used in the examples of producing the reconstructed polypeptides. Hybridomas MABL-1 and MABL-2 producing them respectively were internationally deposited as FERM BP-6100 and FERM BP-6101 with the National Institute of Bioscience and Human Technology, Agency of Industrial Science and Technology, Minister of International Trade and Industry (1-3 Higasi 1-chome, Tsukuba-shi, Ibaraki-ken, Japan), an authorized depository for microorganisms, on Sep. 11, 1997.

EXAMPLE 1

Cloning of DNAs Encoding V Region of Mouse Monoclonal Antibodies to Human IAP

DNAs encoding variable regions of the mouse monoclonal antibodies to human IAP, MABL-1 and MABL-2, were cloned as follows.

1.1 Preparation of Messenger RNA (mRNA)

mRNAs of the hybridomas MABL-1 and MABL-2 were obtained by using mRNA Purification Kit (Pharmacia Biotech).

1.2 Synthesis of Double-Stranded cDNA

Double-stranded cDNA was synthesized from about 1 µg of the mRNA using Marathon cDNA Amplification Kit (CLONTECH) and an adapter was linked thereto.

1.3 PCR Amplification of Genes Encoding Variable Regions of an Antibody by

PCR was carried out using Thermal Cycler (PERKIN ELMER).

(1) Amplification of a Gene Coding for L Chain V Region of MABL-1

Primers used for the PCR method are Adapter Primer-1 (CLONTECH) shown in SEQ ID No. 1, which hybridizes to a partial sequence of the adapter, and MKC (Mouse Kappa Constant) primer (Bio/Technology, 9, 88-89, 1991) shown in SEQ ID No. 2, which hybridizes to the mouse kappa type L chain V region.

50 µl of the PCR solution contains 5 µl of 10×PCR Buffer II, 2 mM MgCl₂, 0.16 mM dNTPs (dATP, dGTP, dCTP and dTTP), 2.5 units of a DNA polymerase, AmpliTaq Gold (PERKIN ELMER), 0.2 µM of the adapter primer of SEQ ID No. 1, 0.2 µM of the MKC primer of SEQ ID No. 2 and 0.1 µg of the double-stranded cDNA derived from MABL-1. The solution was preheated at 94° C. of the initial temperature for 9 minutes and then heated at 94° C. for 1 minute, at 60° C. for 1 minute and at 72° C. for 1 minute 20 seconds in order. This temperature cycle was repeated 35 times and then the reaction mixture was further heated at 72° C. for 10 minutes.

(2) Amplification of cDNA Encoding H Chain V Region of MABL-1

The Adapter Primer-1 shown in SEQ ID No. 1 and MHC-γ1 (Mouse Heavy Constant) primer (Bio/Technology, 9, 88-89, 1991) shown in SEQ ID No. 3 were used as primers for PCR.

The amplification of cDNA was performed according to the method of the amplification of the L chain V region gene, which was described in Example 1.3-(1), except for using 0.2 µM of the MHC-γ1 primer instead of 0.2 µM of the MKC primer.

(3) Amplification of cDNA Encoding L Chain V Region of MABL-2

The Adapter Primer-1 of SEQ ID No. 1 and the MKC primer of SEQ ID No. 2 were used as primers for PCR.

The amplification of cDNA was carried out according to the method of the amplification of the L chain V region gene of MABL-1 which was described in Example 1.3-(1), except for using 0.1 µg of the double-stranded cDNA derived from MABL-2 instead of 0.1 µg of the double-stranded cDNA from MABL-1.

(4) Amplification of cDNA Encoding H Chain V Region of MABL-2

The Adapter Primer-1 of SEQ ID No. 1 and MHC-γ2a primer (Bio/Technology, 9, 88-89, 1991) shown in SEQ ID No. 4 were used as primers for PCR.

The amplification of cDNA was performed according to the method of the amplification of the L chain V region gene, which was described in Example 1.3-(3), except for using 0.2 µM of the MHC-γ2a primer instead of 0.2 µM of the MKC primer.

1.4 Purification of PCR Products

The DNA fragment amplified by PCR as described above was purified using the QIAquick PCR Purification Kit (QIAGEN) and dissolved in 10 mM Tris-HCl (pH 8.0) containing 1 mM EDTA.

1.5 Ligation and Transformation

About 140 ng of the DNA fragment comprising the gene encoding the mouse kappa type L chain V region derived from MABL-1 as prepared above was ligated with 50 ng of pGEM-T Easy vector (Promega) in the reaction buffer comprising 30 mM Tris-HCl (pH 7.8), 10 mM MgCl₂, 10 mM

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dithiothreitol, 1 mM ATP and 3 units of T4 DNA Ligase (Promega) at 15° C. for 3 hours.

Then, 1 µl of the reaction mixture was added to 50 µl of *E. coli* DH5α competent cells (Toyobo Inc.) and the cells were stored on ice for 30 minutes, incubated at 42° C. for 1 minute and stored on ice for 2 minutes again. 100 µl of SOC medium (GIBCO BRL) was added. The cells of *E. coli* were plated on LB (Molecular Cloning: A Laboratory Manual, Sambrook et al., Cold Spring Harbor Laboratory Press, 1989) agar medium containing 100 µg/ml of ampicillin (SIGMA) and cultured at 37° C. overnight to obtain the transformant of *E. coli*.

The transformant was cultured in 3 ml of LB medium containing 50 µg/ml of ampicillin at 37° C. overnight and the plasmid DNA was prepared from the culture using the QIAprep Spin Miniprep Kit (QIAGEN).

The resulting plasmid comprising the gene encoding the mouse kappa type L chain V region derived from the hybridoma MABL-1 was designated as pGEM-M1L.

According to the same manner as described above, a plasmid comprising the gene encoding the mouse H chain V region derived from the hybridoma MABL-1 was prepared from the purified DNA fragment and designated as pGEM-M1H.

A plasmid comprising the gene encoding the mouse kappa type L chain V region derived from the hybridoma MABL-2 was prepared from the purified DNA fragment and designated as pGEM-M2L.

A plasmid comprising the gene encoding the mouse H chain V region derived from the hybridoma MABL-2 was prepared from the purified DNA fragment and designated as pGEM-M2H.

EXAMPLE 2

DNA Sequencing

The nucleotide sequence of the cDNA encoding region in the aforementioned plasmids was determined using Auto DNA Sequencer (Applied Biosystem) and ABI PRISM Dye Terminator Cycle Sequencing Ready Reaction Kit (Applied Biosystem) according to the manufacturer's protocol.

The nucleotide sequence of the gene encoding the L chain V region from the mouse antibody MABL-1, which is included in the plasmid pGEM-M1L, is shown in SEQ ID NO: 5. Its encoded protein is shown in SEQ ID NO: 90.

The nucleotide sequence of the gene encoding the H chain V region from the mouse antibody MABL-1, which is included in the plasmid pGEM-M1H, is shown in SEQ ID NO: 6. Its encoded protein is shown in SEQ ID NO: 91.

The nucleotide sequence of the gene encoding the L chain V region from the mouse antibody MABL-2, which is included in the plasmid pGEM-M2L, is shown in SEQ ID NO: 7. Its encoded protein is shown in SEQ ID NO: 92.

The nucleotide sequence of the gene encoding the H chain V region from the mouse antibody MABL-2, which is included in the plasmid pGEM-M2H, is shown in SEQ ID NO: 8. Its encoded protein is shown in SEQ ID NO: 93.

EXAMPLE 3

Determination of CDR

The V regions of L chain and H chain generally have a similarity in their structures and each four framework regions therein are linked by three hypervariable regions, i.e., complementarity determining regions (CDR). An amino acid sequence of the framework is relatively well conserved, while

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an amino acid sequence of CDR has extremely high variation (Kabat, E. A., et al., "Sequences of Proteins of Immunological Interest", US Dept. Health and Human Services, 1983).

On the basis of these facts, the amino acid sequences of the variable regions from the mouse monoclonal antibodies to human IAP were applied to the database of amino acid sequences of the antibodies made by Kabat et al. to investigate the homology. The CDR regions were determined based on the homology as shown in Table 1.

TABLE 1

15 Plasmid	SEQ ID	SEQ ID No.	CDR (1)	CDR (2)	CDR (3)
	No. (DNA)	(Protein)			
pGEM-M1L	5	90	24-39	55-61	94-102
pGEM-M1H	6	91	31-35	50-66	99-106
pGEM-M2L	7	92	24-39	55-61	94-102
pGEM-M2H	8	93	31-35	50-66	99-106

EXAMPLE 4

Identification of Cloned cDNA Expression
Preparation of Chimera MABL-1 Antibody and
Chimera MABL-2 Antibody

4.1 Preparation of Vectors Expressing Chimera MABL-1 Antibody

cDNA clones, pGEM-M1L and pGEM-M1H, encoding the V regions of the L chain and the H chain of the mouse antibody MABL-1, respectively, were modified by the PCR method and introduced into the HEF expression vector (WO92/19759) to prepare vectors expressing chimera MABL-1 antibody.

A forward primer MLS (SEQ ID No. 9) for the L chain V region and a forward primer MHS (SEQ ID No. 10) for the H chain V region were designed to hybridize to a DNA encoding the beginning of the leader sequence of each V region and to contain the Kozak consensus sequence (J. Mol. Biol., 196, 947-950, 1987) and HindIII restriction enzyme site. A reverse primer MLAS (SEQ ID No. 11) for the L chain V region and a reverse primer MHAS (SEQ ID No. 12) for the H chain V region were designed to hybridize to a DNA encoding the end of the J region and to contain the splice donor sequence and BamHI restriction enzyme site.

100 µl of a PCR solution comprising 10 µl of 10xPCR Buffer II, 2 mM MgCl₂, 0.16 mM dNTPs (dATP, dGTP, dCTP and dTTP), 5 units of DNA polymerase AmpliTaq Gold, 0.4 µM each of primers and 8 ng of the template DNA (pGEM-M1L or pGEM-M1H) was preheated at 94° C. of the initial temperature for 9 minutes and then heated at 94° C. for 1 minute, at 60° C. for 1 minute and at 72° C. for 1 minute 20 seconds in order. This temperature cycle was repeated 35 times and then the reaction mixture was further heated at 72° C. for 10 minutes.

The PCR product was purified using the QIAquick PCR Purification Kit (QIAGEN) and then digested with HindIII and BamHI. The product from the L chain V region was cloned into the HEF expression vector, HEF-κ and the product from the H chain V region was cloned into the HEF expression vector, HEF-γ. After DNA sequencing, plasmids containing a DNA fragment with a correct DNA sequence are designated as HEF-M1L and HEF-M1H, respectively.

4.2 Preparation of Vectors Expressing Chimera MABL-2 Antibodies

Modification and cloning of cDNA were performed in the same manner described in Example 4.1 except for using pGEM-M2L and pGEM-M2H as template DNA instead of pGEM-M1L and pGEM-M1H. After DNA sequencing, plasmids containing DNA fragments with correct DNA sequences are designated as HEF-M2L and HEF-M2H, respectively.

4.3 Transfection to COS7 Cells

The aforementioned expression vectors were tested in COS7 cells to observe the transient expression of the chimera MABL-1 and MABL-2 antibodies.

(1) Transfection with Genes for the Chimera MABL-1 Antibody

COS7 cells were co-transformed with the HEF-M1L and HEF-M1H vectors by electroporation using the Gene Pulser apparatus (BioRad). Each DNA (10 µg) and 0.8 ml of PBS with 1×10^7 cells/ml were added to a cuvette. The mixture was treated with pulse at 1.5 kV, 25 µF of electric capacity.

After the restoration for 10 minutes at a room temperature, the electroporated cells were transferred into DMEM culture medium (GIBCO BRL) containing 10% γ -globulin-free fetal bovine serum. After culturing for 72 hours, the supernatant was collected, centrifuged to remove cell fragments and recovered.

(2) Transfection with Genes Coding for the Chimera MABL-2 Antibody

The co-transfection to COS7 cells with the genes coding for the chimera MABL-2 antibody was carried out in the same manner as described in Example 4.3-(1) except for using the HEF-M2L and HEF-M2H vectors instead of the HEF-M1L and HEF-M1H vectors. The supernatant was recovered in the same manner.

4.4 Flow Cytometry

Flow cytometry was performed using the aforementioned culture supernatant of COS7 cells to measure binding to the antigen. The culture supernatant of the COS7 cells expressing the chimera MABL-1 antibody or the COS7 cells expressing the chimera MABL-2 antibody, or human IgG antibody (SIGMA) as a control was added to 4×10^5 cells of mouse leukemia cell line L1210 expressing human IAP and incubated on ice. After washing, the FITC-labeled anti-human IgG antibody (Cappel) was added thereto. After incubating and washing, the fluorescence intensity thereof was measured using the FACScan apparatus (BECTON DICKINSON).

Since the chimera MABL-1 and MABL-2 antibodies were specifically bound to L1210 cells expressing human IAP, it is confirmed that these chimera antibodies have proper structures of the V regions of the mouse monoclonal antibodies MABL-1 and MABL-2, respectively (FIGS. 1-3).

EXAMPLE 5

Preparation of Reconstructed Single-Chain Fv (scFv) of the Antibody MABL-1 and Antibody MABL-2

5.1 Preparation of Reconstructed Single-Chain Fv of Antibody MABL-1

The reconstructed single-chain Fv of antibody MABL-1 was prepared as follows. The H chain V region and the L chain V of antibody MABL-1, and a linker were respectively amplified by the PCR method and were connected to produce the reconstructed single-chain Fv of antibody MABL-1. The pro-

duction method is illustrated in FIG. 4. Six primers (A-F) were employed for the production of the single-chain Fv of antibody MABL-1. Primers A, C and E have a sense sequence and primers B, D and F have an antisense sequence.

The forward primer VHS for the H chain v region (Primer A, SEQ ID No. 13) was designed to hybridize to a DNA encoding the N-terminal of the H chain V region and to contain NcoI restriction enzyme recognition site. The reverse primer VHAS for H chain V region (Primer B, SEQ ID No. 14) was designed to hybridize to a DNA coding the C-terminal of the H chain V region and to overlap with the linker.

The forward primer LS for the linker (Primer C, SEQ ID No. 15) was designed to hybridize to a DNA encoding the N-terminal of the linker and to overlap with a DNA encoding the C-terminal of the H chain V region. The reverse primer LAS for the linker (Primer D, SEQ ID No. 16) was designed to hybridize to a DNA encoding the C-terminal of the linker and to overlap with a DNA encoding the N-terminal of the L chain V region.

The forward primer VLS for the L chain V region (Primer E, SEQ ID No. 17) was designed to hybridize to a DNA encoding the C-terminal of the linker and to overlap with a DNA encoding the N-terminal of the L chain V region. The reverse primer VLAS-FLAG for L chain V region (Primer F, SEQ ID No. 18) was designed to hybridize to a DNA encoding the C-terminal of the L chain V region and to have a sequence encoding the FLAG peptide (Hopp, T. P. et al., Bio/Technology, 6, 1204-1210, 1988), two stop codons and EcoRI restriction enzyme recognition site.

In the first PCR step, three reactions, A-B, C-D and E-F, were carried out and PCR products thereof were purified. Three PCR products obtained from the first PCR step were assembled by their complementarity. Then, the primers A and F were added and the full length DNA encoding the reconstructed single-chain Fv of antibody MABL-1 was amplified (Second PCR). In the first PCR, the plasmid pGEM-M1H encoding the H chain V region of antibody MABL-1 (see Example 2), a plasmid pSC-DP1 which comprises a DNA sequence (SEQ ID NO: 19) encoding a linker region comprising: Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Gly Gly Gly Ser (SEQ ID NO: 94) (Huston, J. S., et al., Proc. Natl. Acad. Sci. USA, 85, 5879-5883, 1988) and the plasmid pGEM-M1L encoding the L chain V region of antibody MABL-1 (see Example 2) were employed as template, respectively.

50 µl of the solution for the first PCR step comprises 5 µl of 10×PCR Buffer II, 2 mM MgCl₂, 0.16 mM dNTPs, 2.5 units of DNA polymerase, AmpliTaq Gold (PERKIN ELMER), 0.4 µM each of primers and 5 ng each of template DNA. The PCR solution was preheated at 94° C. of the initial temperature for 9 minutes and then heated at 94° C. for 1 minute, at 65° C. for 1 minute and at 72° C. for 1 minute and 20 seconds in order. This temperature cycle was repeated 35 times and then the reaction mixture was further heated at 72° C. for 7 minutes.

The PCR products A-B (371 bp), C-D (63 bp) and E-F (384 bp) were purified using the QIAquick PCR Purification Kit (QIAGEN) and were assembled in the second PCR. In the second PCR, 98 µl of a PCR solution comprising 120 ng of the first PCR product A-B, 20 ng of the PCR product C-D and 120 ng of the PCR product E-F, 10 µl of 10×PCR Buffer II, 2 mM MgCl₂, 0.16 mM dNTPs, 5 units of DNA polymerase AmpliTaq Gold (PERKIN ELMER) was preheated at 94° C. of the initial temperature for 8 minutes and then heated at 94° C. for 2 minutes, at 65° C. for 2 minutes and at 72° C. for 2 minutes in order. This temperature cycle was repeated twice and then 0.4 µM each of primers A and F were added into the reaction,

respectively. The mixture was preheated at 94° C. of the initial temperature for 1 minutes and then heated at 94° C. for 1 minute, at 65° C. for 1 minute and at 72° C. for 1 minute and 20 seconds in order. This temperature cycle was repeated 35 times and then the reaction mixture was further heated at 72° C. for 7 minutes.

A DNA fragment of 843 bp produced by the second PCR was purified and digested by NcoI and EcoRI. The resultant DNA fragment was cloned into pSCFVT7 vector. The expression vector pSCFVT7 contains a pelB signal sequence suitable for *E. coli* periplasmic expression system (Lei, S. P., et al., J. Bacteriology, 169, 4379-4383, 1987). After the DNA sequencing, the plasmid containing the DNA fragment encoding correct amino acid sequence of the reconstructed single-chain Fv of antibody MABL-1 is designated as "pscM1" (see FIG. 5). The nucleotide sequence and the amino acid sequence of the reconstructed single-chain Fv of antibody MABL-1 contained in the plasmid pscM1 are shown in SEQ ID No. 20. The corresponding amino acid sequence is shown in SEQ ID NO. 95.

The pscM1 vector was modified by the PCR method to prepare a vector expressing the reconstructed single-chain Fv of antibody MABL-1 in mammalian cells. The resultant DNA fragment was introduced into pCHO1 expression vector. This expression vector, pCHO1, was constructed by digesting DHFR-ΔE-rvH-PM1-f (WO92/19759) with EcoRI and SmaI to eliminate the antibody gene and connecting the EcoRI-NotI-BamHI Adapter (Takara Shuzo) thereto.

As a forward primer for PCR, Sal-VHS primer shown in SEQ ID No. 21 was designed to hybridize to a DNA encoding the N-terminal of the H chain V region and to contain SalI restriction enzyme recognition site. As a reverse primer for PCR, FRH1anti primer shown in SEQ ID No. 22 was designed to hybridize to a DNA encoding the end of the first framework sequence.

100 μl of PCR solution comprising 10 μl of 10×PCR Buffer II, 2 mM MgCl₂, 0.16 mM dNTPs, 5 units of the DNA polymerase, AmpliTaq Gold, 0.4 μM each of primer and 8 ng of the template DNA (pscM1) was preheated at 95° C. of the initial temperature for 9 minutes and then heated at 95° C. for 1 minute, at 60° C. for 1 minute and at 72° C. for 1 minute and 20 seconds in order. This temperature cycle was repeated 35 times and then the reaction mixture was further heated at 72° C. for 7 minutes.

The PCR product was purified using the QIAquick PCR Purification Kit (QIAGEN) and digested by SalI and MboII to obtain a DNA fragment encoding the N-terminal of the reconstructed single-chain Fv of antibody MABL-1. The pscM1 vector was digested by MboII and EcoRI to obtain a DNA fragment encoding the C-terminal of the reconstructed single-chain Fv of antibody MABL-1. The SalI-MboII DNA fragment and the MboII-EcoRI DNA fragment were cloned into pCHO1-Igs vector. After DNA sequencing, the plasmid comprising the desired DNA sequence was designated as "pCHOM1" (see FIG. 6). The expression vector, pCHO1-Igs, contains a mouse IgG1 signal sequence suitable for the secretion-expression system in mammalian cells (Nature, 322, 323-327, 1988). The nucleotide sequence and the amino acid sequence of the reconstructed single-chain Fv of antibody MABL-1 contained in the plasmid pCHOM1 are shown in SEQ ID No. 23. The corresponding amino acid sequence is shown in SEQ ID NO. 96.

5.2 Preparation of Reconstructed Single-Chain Fv of Antibody MABL-2

The reconstructed single-chain Fv of antibody MABL-2 was prepared in accordance with the aforementioned

Example 5.1. Employed in the first PCR step were plasmid pGEM-M2H encoding the H chain V region of MABL-2 (see Example 2) instead of pGEM-M1H and plasmid pGEM-M2L encoding the L chain V region of MABL-2 (see Example 2) instead of pGEM-M1L, to obtain a plasmid pscM2 which comprises a DNA fragment encoding the desired amino acid sequence of the single-chain Fv of antibody MABL-2. The nucleotide sequence and the amino acid sequence of the reconstructed single-chain Fv of antibody MABL-2 contained in the plasmid pscM2 are shown in SEQ ID No. 24. The corresponding amino acid sequence is shown in SEQ ID NO. 97.

The pscM2 vector was modified by the PCR method to prepare a vector, pCHOM2, for the expression in mammalian cells which contains the DNA fragment encoding the correct amino acid sequence of reconstructed the single-chain Fv of antibody MABL-2. The nucleotide sequence and the amino acid sequence of the reconstructed single-chain Fv of antibody MABL-2 contained in the plasmid pCHOM2 are shown in SEQ ID No. 25. The corresponding amino acid sequence is shown in SEQ ID NO. 98.

5.3 Transfection to COS7 Cells

The pCHOM2 vector was tested in COS7 cells to observe the transient expression of the reconstructed single-chain Fv of antibody MABL-2.

The COS7 cells were transformed with the pCHOM2 vector by electroporation using the Gene Pulser apparatus (Bio-Rad). The DNA (10 μg) and 0.8 ml of PBS with 1×10⁷ cells/ml were added to a cuvette. The mixture was treated with pulse at 1.5 kV, 25 μF of electric capacity.

After the restoration for 10 minutes at a room temperature, the electroporated cells were transferred into IMDM culture medium (GIBCO BRL) containing 10% fetal bovine serum. After culturing for 72 hours, the supernatant was collected, centrifuged to remove cell fragments and recovered.

5.4 Detection of the Reconstructed Single-Chain Fv of Antibody MABL-2 in Culture Supernatant of COS7 Cells

The existence of the single-chain Fv of antibody MABL-2 in the culture supernatant of COS7 cells which had been transfected with the pCHOM2 vector was confirmed by the Western Blotting method.

The culture supernatant of COS7 cells transfected with the pCHOM2 vector and the culture supernatant of COS7 cells transfected with the pCHO1 as a control were subjected to SDS electrophoresis and transferred to REINFORCED NC membrane (Schleicher & Schuell). The membrane was blocked with 5% skim milk (Morinaga Nyu-gyo), washed with 0.05% Tween 20-PBS and mixed with an anti-FLAG antibody (SIGMA). The membrane was incubated at room temperature, washed and mixed with alkaline phosphatase-conjugated mouse IgG antibody (Zymed). After incubating and washing at room temperature, the substrate solution (Kirkegaard Perry Laboratories) was added to develop color (FIG. 7).

A FLAG-peptide-specific protein was detected only in the culture supernatant of the pCHOM2 vector-introduced COS7 cells and thus it is confirmed that the reconstructed single-chain Fv of antibody MABL-2 was secreted in this culture supernatant.

5.5 Flow Cytometry

Flow cytometry was performed using the aforementioned COS7 cells culture supernatant to measure the binding to the antigen. The culture supernatant of the COS7 cells expressing the reconstructed single-chain Fv of antibody MABL-2 or the culture supernatant of COS7 cells transformed with pCHO1

vector as a control was added to 2×10^5 cells of the mouse leukemia cell line L1210 expressing human Integrin Associated Protein (IAP) or the cell line L1210 transformed with pCOS1 as a control. After incubating on ice and washing, the mouse anti-FLAG antibody (SIGMA) was added. Then the cells were incubated and washed. Then, the FITC labeled anti-mouse IgG antibody (BECTON DICKINSON) was added thereto and the cells were incubated and washed again. Subsequently, the fluorescence intensity was measured using the FACScan apparatus (BECTON DICKINSON).

Since the single-chain Fv of antibody MABL-2 was specifically bound to L1210 cells expressing human IAP, it is confirmed that the reconstructed single-chain Fv of antibody MABL-2 has an affinity to human Integrin Associated Protein (IAP) (see FIGS. 8-11).

5.6 Competitive ELISA

The binding activity of the reconstructed single-chain Fv of antibody MABL-2 was measured based on the inhibiting activity against the binding of mouse monoclonal antibodies to the antigen.

The anti-FLAG antibody adjusted to 1 $\mu\text{g/ml}$ was added to each well on 96-well plate and incubated at 37° C. for 2 hours. After washing, blocking was performed with 1% BSA-PBS. After incubating and washing at a room temperature, the culture supernatant of COS7 cells into which the secretion-type human TAP antigen gene (see SEQ ID NOS 26 and 99) had been introduced was diluted with PBS into twofold volume and added to each well. After incubating and washing at a room temperature, a mixture of 50 μl of the biotinized MABL-2 antibody adjusted to 100 ng/ml and 50 μl of sequentially diluted supernatant of the COS7 cells expressing the reconstructed single-chain Fv of antibody MABL-2 were added into each well. After incubating and washing at a room temperature, the alkaline phosphatase-conjugated streptavidin (Zymed) was added into each well. After incubating and washing at a room temperature, the substrate solution (SIGMA) was added and absorbance of the reaction mixture in each well was measured at 405 nm.

The results revealed that the reconstructed single-chain Fv of antibody MABL-2 (MABL2-scFv) evidently inhibited concentration-dependently the binding of the mouse antibody MABL-2 to human IAP antigen in comparison with the culture supernatant of the PCHO1-introduced COS7 cells as a control (FIG. 12). Accordingly, it is suggested that the reconstructed single-chain Fv of antibody MABL-2 has the correct structure of each of the V regions from the mouse monoclonal antibody MABL-2.

5.7 Apoptosis-Inducing Effect in Vitro

An apoptosis-inducing action of the reconstructed single-chain Fv of antibody MABL-2 was examined by Annexin-V staining (Boehringer Mannheim) using the L1210 cells transfected with human IAP gene, the L1210 cells transfected with the pCOS1 vector as a control and CCRF-CEM cells.

To each 1×10^5 cells of the above cells was added the culture supernatant of the COS7 cells expressing the reconstructed single-chain Fv of antibody MABL-2 or the culture supernatant of COS7 cells transfected with the pCHO1 vector as a control at 50% final concentration and the mixtures were cultured for 24 hours. Then, the Annexin-V staining was performed and the fluorescence intensity was measured using the FACScan apparatus (BECTON DICKINSON).

Results of the Annexin-V staining are shown in FIGS. 13-18, respectively. Dots in the left-lower region represent living cells and dots in the right-lower region represent cells at the early stage of apoptosis and dots in the right-upper region represent cells at the late stage of apoptosis. The results

show that the reconstructed single-chain Fv of antibody MABL-2 (MABL2-scFv) remarkably induced cell death of L1210 cells specific to human IAP antigen (FIGS. 13-16) and that the reconstructed single-chain Fv also induced remarkable cell death of CCRF-CEM cells in comparison with the control (FIGS. 17-18).

5.8 Expression of MABL-2 Derived Single-Chain Fv in CHO Cells

CHO cells were transfected with the pCHOM2 vector to establish a CHO cell line which constantly expresses the single-chain Fv (polypeptide) derived from the antibody MABL-2.

CHO cells were transformed with the pCHOM2 vector by the electroporation using the Gene Pulser apparatus (Bio-Rad). A mixture of DNA (10 μg) and 0.7 ml of PBS with CHO cells (1×10^7 cells/ml) was added to a cuvette. The mixture was treated with pulse at 1.5 kV, 25 μF of electric capacity. After the restoration for 10 minutes at a room temperature, the electroporated cells were transferred into nucleic acid free α -MEM medium (GIBCO BRL) containing 10% fetal bovine serum and cultured. The expression of desired protein in the resultant clones was confirmed by SDS-PAGE and a clone with a high expression level was selected as a cell line producing the single-chain Fv derived from the antibody MABL-2. The cell line was cultured in serum free medium CHO-S-SFM II (GIBCO BRL) containing 10 nM methotrexate (SIGMA). Then, the culture supernatant was collected, centrifuged to remove cell fragments and recovered.

5.9 Purification of MABL-2 Derived Single-Chain Fv Produced in CHO Cells

The culture supernatant of the CHO cell line expressing the single-chain Fv obtained in Example 5.8 was concentrated up to twenty times using a cartridge for the artificial dialysis (PAN130SF, ASAHIMEDICALS). The concentrated solution was stored at -20° C. and thawed on purification.

Purification of the single-chain Fv from the culture supernatant of the CHO cells was performed using three kinds of chromatography, i.e., Blue-sepharose, a hydroxyapatite and a gel filtration.

(1) Blue-Sepharose Column Chromatography

The concentrated supernatant was diluted to ten times with 20 mM acetate buffer (pH 6.0) and centrifuged to remove insoluble materials (10000 \times rpm, 30 minutes). The supernatant was applied onto a Blue-sepharose column (20 ml) equilibrated with the same buffer. After washing the column with the same buffer, proteins adsorbed in the column were eluted by a stepwise gradient of NaCl in the same buffer, 0.1, 0.2, 0.3, 0.5 and up to 1.0 M. The pass-through fraction and each eluted fraction were analyzed by SDS-PAGE. The fractions in which the single-chain Fv were confirmed (the fractions eluted at 0.1 to 0.3M NaCl) were pooled and concentrated up to approximately 20 times using CentriPrep-10 (AMICON).

(2) Hydroxyapatite

The concentrated solution obtained in (1) was diluted to 10 times with 10 mM phosphate buffer (pH 7.0) and applied onto the hydroxyapatite column (20 ml, BIORAD). The column was washed with 60 ml of 10 mM phosphate buffer (pH 7.0). Then, proteins adsorbed in the column were eluted by a linear gradient of sodium phosphate buffer up to 200 mM (see FIG. 19). The analysis of each fraction by SDS-PAGE confirmed the single-chain Fv in fraction A and fraction B.

(3) Gel Filtration

Each of fractions A and B in (2) was separately concentrated with CentriPrep-10 and applied onto TSKgel G3000SWG column (21.5×600 mm) equilibrated with 20 mM acetate buffer (pH 6.0) containing 0.15 M NaCl. Chromatograms are shown in FIG. 20. The analysis of the fractions by SDS-PAGE confirmed that both major peaks (AI and BI) are of desired single-chain Fv. In the gel filtration analysis, the fraction A was eluted at 36 kDa of apparent molecular weight and the fraction B was eluted at 76 kDa. The purified single-chain Fvs (AI, BI) were analyzed with 15% SDS polyacrylamide gel. Samples were treated in the absence or presence of a reductant and the electrophoresis was carried out in accordance with the Laemmli's method. Then the protein was stained with Coomassie Brilliant Blue. As shown in FIG. 21, both AI and BI gave a single band at 35 kDa of apparent molecular weight, regardless of the absence or presence of the reductant. From the above, it is concluded that AI is a monomer of the single-chain Fv and BI is a non-covalently bound dimer of the single-chain Fv. The gel filtration analysis of the fractions AI and BI with TSKgel G3000SW column (7.5×60 mm) revealed that a peak of the monomer is detected only in the fraction AI and a peak of the dimer is detected only in the fraction BI (FIG. 22). The dimer fraction (fraction BI) accounted for 4 percent (%) of total single-chain Fvs. More than 90% of the dimer in the dimer fraction was stably preserved for more than a month at 40° C.

5.10 Construction of Vector Expressing Single-Chain Fv Derived from Antibody MABL-2 in *E. Coli* Cell

The pscM2 vector was modified by the PCR method to prepare a vector effectively expressing the single-chain Fv from the antibody MABL-2 in *E. coli* cells. The resultant DNA fragment was introduced into pSCFVT7 expression vector.

As a forward primer for PCR, Nde-VHSm02 primer shown in SEQ ID No. 27 was designed to hybridize to a DNA encoding the N-terminal of the H chain V region and to contain a start codon and NdeI restriction enzyme recognition site. As a reverse primer for PCR, VLAS primer shown in SEQ ID No. 28 was designed to hybridize to a DNA encoding the C-terminal of the L chain V region and to contain two stop codons and EcoRI restriction enzyme recognition site. The forward primer, Nde-VHSm02, comprises five point mutations in the part hybridizing to the DNA encoding the N-terminal of the H chain V region for the effective expression in *E. coli*.

100 µl of a PCR solution comprising 10 µl of 10×PCR Buffer #1, 1 mM MgCl₂, 0.2 mM dNTPs, 5 units of KOD DNA polymerase (all from TOYOBO), 1 µM of each primer and 100 ng of a template DNA (pscM2) was heated at 98° C. for 15 seconds, at 65° C. for 2 seconds and at 74° C. for 30 seconds in order. This temperature cycle was repeated 25 times.

The PCR product was purified using the QIAquick PCR Purification Kit (QIAGEN) and digested by NdeI and EcoRI, and then the resulting DNA fragment was cloned into pSCFVT7 vector, from which pelB signal sequence had been eliminated by the digestion with NdeI and EcoRI. After DNA sequencing, the resulting plasmid comprising a DNA fragment with the desired DNA sequence is designated as "pscM2DEm02" (see FIG. 23). The nucleotide sequence and the amino acid sequence of the single-chain Fv derived from the antibody MABL-2 contained in the plasmid pscM2DEm02 are shown in SEQ ID No. 29. The corresponding amino acid sequence is shown in SEQ ID NO. 100.

5.11 Expression of Single-Chain Fv Derived from Antibody MABL-2 in *E. Coli* Cells

E. coli BL21(DE3)pLysS (STRATAGENE) was transformed with pscM2DEm02 vector to obtain a strain of *E. coli* expressing the single-chain Fv derived from antibody MABL-2. The resulting clones were examined for the expression of the desired protein using SDS-PAGE, and a clone with a high expression level was selected as a strain producing the single-chain Fv derived from antibody MABL-2.

5.12 Purification of Single-Chain Fv Derived from Antibody MABL-2 Produced in *E. Coli*

A single colony of *E. coli* obtained by the transformation was cultured in 3 ml of LB medium at 28° C. for 7 hours and then in 70 ml of LB medium at 28° C. overnight. This pre-culture was transplanted to 7 L of LB medium and cultured at 28° C. with stirring at 300 rpm using the Jar-fermenter. When an absorbance of the medium reached O.D.=1.5, the bacteria were induced with 1 mM IPTG and then cultured for 3 hours.

The culture medium was centrifuged (10000×g, 10 minutes) and the precipitated bacteria were recovered. To the bacteria was added 50 mM Tris-HCl buffer (pH 8.0) containing 5 mM EDTA, 0.1 M NaCl and 1% Triton X-100 and the bacteria were disrupted by ultrasonication (out put: 4, duty cycle: 70%, 1 minutex10 times). The suspension of disrupted bacteria was centrifuged (12000×g, 10 minutes) to precipitate inclusion body. Isolated inclusion body was mixed with 50 mM Tris-HCl buffer (pH 8.0) containing 5 mM EDTA, 0.1 M NaCl and 4% Triton X-100, treated by ultrasonication (out put: 4, duty cycle: 50%, 30 secondsx2 times) again and centrifuged (12000×g, 10 minutes) to isolate the desired protein as precipitate and to remove containment proteins included in the supernatant.

The inclusion body comprising the desired protein was lysed in 50 mM Tris-HCl buffer (pH 8.0) containing 6 M Urea, 5 mM EDTA and 0.1 M NaCl and applied onto Sephacryl S-300 gel filtration column (5×90 cm, Amersham Pharmacia) equilibrated with 50 mM Tris-HCl buffer (pH 8.0) containing 4M Urea, 5 mM EDTA, 0.1 M NaCl and 10 mM mercaptoethanol at a flow rate of 5 ml/minutes to remove associated single chain Fvs with high-molecular weight. The obtained fractions were analyzed with SDS-PAGE and the fractions with high purity of the protein were diluted with the buffer used in the gel filtration up to O.D₂₈₀=0.25. Then, the fractions were dialyzed three times against 50 mM Tris-HCl buffer (pH 8.0) containing 5 mM EDTA, 0.1 M NaCl, 0.5 M Arg, 2 mM glutathione in the reduced form and 0.2 mM glutathione in the oxidized form in order for the protein to be refolded. Further, the fraction was dialyzed three times against 20 mM acetate buffer (pH 6.0) containing 0.15 M NaCl to exchange the buffer.

The dialysate product was applied onto Superdex 200 µg gel filtration column (2.6×60 cm, Amersham Pharmacia) equilibrated with 20 mM acetate buffer (pH 6.0) containing 0.15 M NaCl to remove a small amount of high molecular weight protein which was intermolecularly crosslinked by S—S bonds. As shown in FIG. 24, two peaks, major and sub peaks, were eluted after broad peaks which are expectedly attributed to an aggregate with a high molecular weight. The analysis by SDS-PAGE (see FIG. 21) and the elution positions of the two peaks in the gel filtration analysis suggest that the major peak is of the monomer of the single-chain Fv and the sub peak is of the non-covalently bound dimer of the single-chain Fv. The non-covalently bound dimer accounted for 4 percent of total single-chain Fvs.

5.13 Apoptosis-Inducing Activity in Vitro of Single-Chain Fv Derived from Antibody MABL-2

An apoptosis-inducing action of the single-chain Fv from antibody MABL-2 (MABL2-scFv) produced by the CHO cells and *E. coli* was examined according to two protocols by

Annexin-V staining (Boehringer Mannheim) using the L1210 cells (hIAP/L1210) into which human IAP gene had been introduced.

In the first protocol sample antibodies at the final concentration of 3 $\mu\text{g/ml}$ were added to 5×10^4 cells of hIAP/L1210 cell line and cultured for 24 hours. Sample antibodies, i.e., the monomer and the dimer of the single-chain Fv of MABL-2 from the CHO cells obtained in Example 5.9, the monomer and the dimer of the single-chain Fv of MABL-2 from *E. coli* obtained in Example 5.12, and the mouse IgG antibody as a control were analyzed. After culturing, the Annexin-V staining was carried out and the fluorescence intensity thereof was measured using the FACScan apparatus (BECTON DICKINSON).

In the second protocol sample antibodies at the final concentration of 3 $\mu\text{g/ml}$ were added to 5×10^4 cells of hIAP/L1210 cell line, cultured for 2 hours and mixed with anti-FLAG antibody (SIGMA) at the final concentration of 15 $\mu\text{g/ml}$ and further cultured for 22 hours. Sample antibodies of the monomer of the single-chain Fv of MABL-2 from the CHO cells obtained in Example 5.9 and the mouse IgG antibody as a control were analyzed. After culturing, the Annexin-V staining was carried out and the fluorescence intensity thereof was measured using the FACScan apparatus.

Results of the analysis by the Annexin-V staining are shown in FIGS. 25-31. The results show that the dimers of the single-chain Fv polypeptide of MABL-2 produced in the CHO cells and *E. coli* remarkably induced cell death (FIGS. 26, 27) in comparison with the control (FIG. 25), while no apoptosis-inducing action was observed in the monomers of the single-chain Fv polypeptide of MABL-2 produced in the CHO cells and *E. coli* (FIGS. 28, 29). When anti-FLAG antibody was used together, the monomer of the single-chain Fv polypeptide derived from antibody MABL-2 produced in the CHO cells induced remarkably cell death (FIG. 31) in comparison with the control (FIG. 30).

5.14 Antitumor Effect of the Monomer and the Dimer of scFv/CHO Polypeptide with a Model Mouse of Human Myeloma

(1) Quantitative Measurement of Human IgG in Mouse Serum

Measurement of human IgG (M protein) produced by human myeloma cell and contained in mouse serum was carried out by the following ELISA. 100 μL of goat anti-human IgG antibody (BIOSOURCE, Lot#7902) diluted to 1 $\mu\text{g/ml}$ with 0.1% bicarbonate buffer (pH 9.6) was added to each well on 96 wells plate (Nunc) and incubated at 4° C. overnight so that the antibody was immobilized. After blocking, 100 μL of the stepwisely diluted mouse serum or human IgG (CAPPEL, Lot#00915) as a standard was added to each well and incubated for 2 hours at a room temperature. After washing, 100 μL of alkaline phosphatase-labeled anti-human IgG antibody (BIOSOURCE, Lot#6202) which had been diluted to 5000 times was added, and incubation was carried out for 1 hour at a room temperature. After washing, a substrate solution was added. After incubation, absorbance at 405 nm was measured using the MICROPLATE READER Model 3550 (BioRad). The concentration of human IgG in the mouse serum was calculated based on the calibration curve obtained from the absorbance values of human IgG as the standard.

(2) Preparation of Antibodies for Administration

The monomer and the dimer of the scFv/CHO polypeptide were respectively diluted to 0.4 mg/mL or 0.25 mg/mL with sterile filtered PBS(-) on the day of administration to prepare samples for the administration.

(3) Preparation of a Mouse Model of Human Myeloma

A mouse model of human myeloma was prepared as follows. KPMM2 cells passaged in vivo (JP-Appl. 7-236475) by SCID mouse (Japan Clare) were suspended in RPMI1640 medium (GIBCO-BRL) containing 10% fetal bovine serum (GIBCO-BRL) and adjusted to 3×10^7 cells/mL. 200 μL of the KPMM2 cell suspension (6×10^6 cells/mouse) was transplanted to the SCID mouse (male, 6 week-old) via caudal vein thereof, which had been subcutaneously injected with the asialo GM1 antibody (WAKO JUNYAKU, 1 vial dissolved in 5 mL) a day before the transplantation.

(4) Administration of Antibodies

The samples of the antibodies prepared in (2), the monomer (250 μL) and the dimer (400 μL), were administered to the model mice of human myeloma prepared in (3) via caudal vein thereof. The administration was started from three days after the transplantation of KPMM2 cells and was carried out twice a day for three days. As a control, 200 μL of sterile filtered PBS(-) was likewise administered twice a day for three days via caudal vein. Each group consisted of seven mice.

(5) Evaluation of Antitumor Effect of the Monomer and the Dimer of scFv/CHO Polypeptide with the Model Mouse of Human Myeloma

The antitumor effect of the monomer and the dimer of scFv/CHO polypeptide with the model mice of human myeloma was evaluated in terms of the change of human IgG (M protein) concentration in the mouse serum and survival time of the mice. The change of human IgG concentration was determined by measuring it in the mouse serum collected at 24 days after the transplantation of KPMM2 cells by ELISA described in the above (1). The amount of serum human IgG (M protein) in the serum of the PBS(-)-administered group (control) increased to about 8500 $\mu\text{g/ml}$, whereas the amount of human IgG of the scFv/CHO dimer-administered group was remarkably low, that is, as low as one-tenth or less than that of the control group. Thus, the results show that the dimer of scFv/CHO strongly inhibits the growth of the KPMM2 cells (FIG. 32). As shown in FIG. 33, a remarkable elongation of the survival time was observed in the scFv/CHO dimer-administered group in comparison with the PBS(-)-administered group.

From the above, it is confirmed that the dimer of scFv/CHO has an antitumor effect for the human myeloma model mice. It is considered that the antitumor effect of the dimer of scFv/CHO, the reconstructed polypeptide of the invention, results from the apoptosis-inducing action of the reconstructed polypeptide.

5.15 Hemagglutination Test

Hemagglutination test and determination of hemagglutination were carried out in accordance with "Immuno-Biochemical Investigation", Zoku-Seikagaku Jikken Koza, edited by the Biochemical Society of Japan, published by Tokyo Kagaku Dojin.

Blood was taken from a healthy donor using heparin-treated syringes and washed with PBS(-) three times, and then erythrocyte suspension with a final concentration of 2% in PBS(-) was prepared. Test samples were the antibody MABL-2, the monomer and the dimer of the single-chain Fv polypeptide produced by the CHO cells, and the monomer

and the dimer of the single-chain Fv polypeptide produced by *E. coli*, and the control was mouse IgG (ZYMED). For the investigation of the hemagglutination effect, round bottom 96-well plates available from Falcon were used. 50 μ L per well of the aforementioned antibody samples and 50 μ L of the 2% erythrocyte suspension were added and mixed in the well. After incubation for 2 hours at 37° C., the reaction mixtures were stored at 4° C. overnight and the hemagglutination thereof was determined. As a control, 50 μ L per well of PBS(-) was used and the hemagglutination test was carried out in the same manner. The mouse IgG and antibody MABL-2 were employed at 0.01, 0.1, 1.0, 10.0 or 100.0 μ g/mL of the final concentration of the antibodies. The single-chain Fvs were employed at 0.004, 0.04, 0.4, 4.0, 40.0 or 80.0 μ g/mL of the final concentration and further at 160.0 μ g/mL only in the case of the dimer of the polypeptide produced by *E. coli*. Results are shown in the Table 2. In the case of antibody MABL-2, the hemagglutination was observed at a concentration of more than 0.1 μ g/mL, whereas no hemagglutination was observed for both the monomer and the dimer of the single-chain Fv.

TABLE 2

H magglutination Test									
	Control	0.01	0.1	1	10	100	μ g/mL		
mIgG	-	-	-	-	-	-	-		
MABL-2 (intact)	-	-	+	+++	+++	++	-		
	Control	0.004	0.04	0.4	4	40	80	μ g/mL	
scFv/CHO monomer	-	-	-	-	-	-	-	-	
scFv/CHO dimer	-	-	-	-	-	-	-	-	
	Control	0.004	0.04	0.4	4	40	80	160	μ g/mL
scFv/ <i>E.coli</i> monomer	-	-	-	-	-	-	-	-	-
scFv/ <i>E.coli</i> dimer	-	-	-	-	-	-	-	-	-

EXAMPLE 6

Reconstructed Polypeptide sc(Fv)₂ Comprising Two H Chain V Regions and Two L Chain V Regions and Antibody MABL-2 scFvs Having Linkers with Different Length

6.1 Construction of Plasmid Expressing Antibody MABL-2 sc(Fv)₂

For the preparation of a plasmid expressing the reconstructed polypeptide [sc(FV)₂] which comprises two H chain V regions and two L chain V regions derived from the antibody MABL-2, the aforementioned pCHOM2, which comprises the DNA encoding scFv derived from the MABL-2 described above, was modified by the PCR method as mentioned below and the resulting DNA fragment was introduced into pCHOM2.

Primers employed for the PCR are EF1 primer (SEQ ID NO: 30) as a sense primer, which is designed to hybridize to a DNA encoding EF1 α , and an antisense primer (SEQ ID NO: 19), which is designed to hybridize to the DNA encoding C-terminal of the L chain V region and to contain a DNA

sequence coding for a linker region, and VLLAS primer containing Sall restriction enzyme recognition site (SEQ ID NO 31).

100 μ l of the PCR solution comprises 10 μ l of 10 \times PCR Buffer #1, 1 mM MgCl₂, 0.2 mM dNTPs (dATP, dGTP, dCTP and dTTP), 5 units of KOD DNA polymerase (Toyobo, Inc.), 1 μ M of each primer and 100 ng of the template DNA (pCHOM2). The PCR solution was heated at 94° C. for 30 seconds, at 50° C. for 30 seconds and at 74° C. for 1 minute in order. This temperature cycle was repeated 30 times.

The PCR product was purified using the QIAquick PCR Purification Kit (QIAGEN) and digested by Sall. The resultant DNA fragment was cloned into pBluescript KS.sup.+ vector (Toyobo, Inc.). After DNA sequencing, a plasmid comprising the desired DNA sequence was digested by Sall and the obtained DNA fragment was connected using Rapid DNA Ligation Kit (BOEHRINGER MANNHEIM) to pCHOM2 digested by Sall. After DNA sequencing, a plasmid comprising the desired DNA sequence is designated as "pCHOM2 (Fv).sub.2" (see FIG. 34). The nucleotide sequence and the amino acid sequence of the antibody MABL-2 sc(Fv).sub.2

region contained in the plasmid pCHOM2(Fv).sub.2 are shown in SEQ ID No. 32. The corresponding amino acid sequence is shown in SEQ ID NO. 101.

6.2 Preparation of Plasmid Expressing Antibody MABL-2 scFvs Having Linkers with Various Length

The scFvs containing linkers with different length and the V regions which are designed in the order of [H chain]-[L chain] (hereinafter "HL") or [L chain]-[H chain] (hereinafter "LH") were prepared using, as a template, cDNAs encoding the H chain and the L chain derived from the MABL-2 as mentioned below.

To construct HL type scFv the PCR procedure was carried out using pCHOM2(Fv)₂ as a template. In the PCR step, a pair of CFHL-F1 primer (SEQ ID NO: 33) and CFHL-R2 primer (SEQ ID NO: 34) or a pair of CFHL-F2 primer (SEQ ID NO: 35) and CFHL-R1 primer (SEQ ID NO: 36) and KOD polymerase were employed. The PCR procedure was carried out by repeating 30 times the temperature cycle consisting of 94° C. for 30 seconds, 60° C. for 30 seconds and 72° C. for 1 minute in order to produce a cDNA for the H chain containing a leader sequence at 5'-end or a cDNA for the L chain containing FLAG sequence at 3'-end thereof. The resultant cDNAs for the H chain and the L chain were mixed and PCR

was carried out by repeating 5 times the temperature cycle consisting of 94° C. for 30 seconds, 60° C. for 30 seconds and 72° C. for 1 minute in order using the mixture as templates and the KOD polymerase. To the reaction mixture were added CFHL-F1 and CFHL-R1 primers and then the PCR reaction was performed by repeating 30 times of the aforementioned temperature cycle to produce a cDNA for HL-0 type without a linker.

To construct LH type scFv, the PCR reaction was carried out using, as a template, pGEM-M2L and pGEM-M2H which contain cDNAs encoding the L chain V region and the H chain V region from the antibody MABL-2, respectively (see JP-Appl. 11-63557). A pair of T7 primer (SEQ ID NO: 37) and CFLH-R2 primer (SEQ ID NO: 38) or a pair of CFLH-F2 primer (SEQ ID NO: 39) and CFLH-R1 (SEQ ID NO: 40) and the KOD polymerase (Toyobo Inc.) were employed. The PCR reaction was performed by repeating 30 times the temperature cycle consisting of 94° C. for 30 seconds, 60° C. for 30 seconds and 72° C. for 1 minute in sequential order to produce a cDNA of an L chain containing a leader sequence at 5'-end or a cDNA of an H chain containing FLAG sequence at 3'-end thereof. The resultant cDNAs of the L chain and the H chain were mixed and PCR was carried out using this mixture as templates and the KOD polymerase by repeating 5 times the temperature cycle consisting of 94° C. for 30 seconds, 60° C. for 30 seconds and 72° C. for 1 minute in order. To the reaction mixture were added T7 and CFLH-R1 primers and the reaction was performed by repeating 30 times of the aforementioned temperature cycle. The reaction product was used as a template and PCR was carried out using a pair of CFLH-F4 primer (SEQ ID NO: 41) and CFLH-R1 primer by repeating 30 times the temperature cycle consisting of 94° C. for 30 seconds, 60° C. for 30 seconds and 72° C. for 1 minute in order to produce a cDNA of LH-0 type without a linker.

The resultant cDNAs of LH-0 and HL-0 types were digested by EcoRI and BamHI restriction enzymes (Takara Shuzo) and the digested cDNAs were introduced into an expression plasmid INPEP4 for mammalian cells using Ligation High (Toyobo Inc.), respectively. Competent *E. coli* JM109 (Nippon Gene) was transformed with each plasmid and the desired plasmids were isolated from the transformed *E. coli* using QIAGEN Plasmid Maxi Kit (QIAGEN). Thus plasmids pCF2LH-0 and pCF2HL-0 were prepared.

To construct the expression plasmids of HL type containing linkers with different size, pCF2HL-0, as a template, and CFHL-X3 (SEQ ID NO: 42), CFHL-X4 (SEQ ID NO: 43), CFHL-X5 (SEQ ID NO: 44), CFHL-X6 (SEQ ID NO: 45) or CFHL-X7 (SEQ ID NO: 46), as a sense primer, and BGH-1 (SEQ ID NO: 47) primer, as an antisense primer, which is complementary with the vector sequence were employed. PCR reaction was carried out using the KOD polymerase by repeating 30 times the temperature cycle consisting of 94° C. for 30 seconds, 60° C. for 30 seconds and 72° C. for 1 minute in order and the reaction products were digested by restriction enzymes XhoI and BamHI (Takara Shuzo). The digested fragments were introduced between XhoI and BamHI sites in the pCF2HL-0 using Ligation High (Toyobo Inc.), respectively. Competent *E. coli* JM109 was transformed with each plasmid and the desired plasmids were isolated from the transformed *E. coli* by using Qiagen Plasmid Maxi kit. Thus expression plasmids pCF2HL-3, pCF2HL-4, pCF2HL-5, pCF2HL-6 and pCF2HL-7 were prepared.

To construct expression plasmid for the transient expression in COS7 cells the plasmids pCF2HL-0, pCF2HL-3, pCF2HL-4, pCF2HL-5, pCF2HL-6 and pCF2HL-7 were digested by restriction enzymes EcoRI and BamHI (Takara Shuzo) and the resultant fragments of approximately 800 bp

were purified with agarose gel electrophoresis. The obtained fragments were introduced between EcoRI and BamHI sites in an expression plasmid pCOS1 for the expression in mammalian cells by using Ligation High (Toyobo Inc.), respectively. Competent *E. coli* DH5 α (Toyobo Inc.) was transformed with each plasmid and the desired plasmids were isolated from the transformed *E. coli* using Qiagen Plasmid Maxi kit. Thus the expression plasmids CF2HL-0/pCOS1, CF2HL-3/pCOS1, CF2HL-4/pCOS1, CF2HL-5/pCOS1, CF2HL-6/pCOS1 and CF2HL-7/pCOS1 were prepared.

As a typical example of these plasmids, the construction of the plasmid CF2HL-0/pCOS1 is illustrated in FIG. 35 and the nucleotide sequence and the amino acid sequence of MABL2-scFv <HL-0> contained in the plasmid are shown in SEQ ID No. 48. Nucleotide sequences and amino acid sequences of the linker regions in these plasmids are also shown in FIG. 36. The corresponding amino acid sequence is shown in SEQ ID NO. 102.

To construct the expression plasmids of LH type containing linkers with different size, pCF2LH-0, as a template, and CFLH-X3 (SEQ ID NO: 49), CFLH-X4 (SEQ ID NO: 50), CFLH-X5 (SEQ ID NO: 51), CFLH-X6 (SEQ ID NO: 52) or CFLH-X7 (SEQ ID NO: 53), as a sense primer, and BGH-1 primer, as an antisense primer, which is complementary with the vector sequence were employed. PCR reaction was carried out using the KOD polymerase by repeating 30 times the temperature cycle consisting of 94° C. for 30 seconds, 60° C. for 30 seconds and 72° C. for 1 minute in order and the reaction products were digested by restriction enzymes XhoI and BamHI. The digested fragments were introduced into the pCF2LH-0 between XhoI and BamHI sites using Ligation High, respectively. Competent *E. coli* DH5 α (Toyobo Inc.) was transformed with each plasmid and the desired plasmids were isolated from the transformed *E. coli* using Qiagen Plasmid Maxi kit. Thus expression plasmids pCF2LH-3, pCF2LH-4, pCF2LH-5, pCF2LH-6 and pCF2LH-7 were prepared.

To construct expression plasmid for the transient expression in COS7 cells the plasmids pCF2LH-0, pCF2LH-3, pCF2LH-4, pCF2LH-5, pCF2LH-6 and pCF2LH-7 were digested by restriction enzymes EcoRI and BamHI (Takara Shuzo) and the resultant fragments of approximately 800 bp were purified with agarose gel electrophoresis. The obtained fragments were introduced between XhoI and BamHI sites in an expression plasmid pCOS1 for the expression in mammalian cells by using the Ligation High, respectively. Competent *E. coli* DH5 α (Toyobo Inc.) was transformed with each plasmid and the desired plasmids were isolated from the transformed *E. coli* using the Qiagen Plasmid Maxi kit. Consequently, the expression plasmids CF2LH-0/pCOS1, CF2LH-3/pCOS1, CF2LH-4/pCOS1, CF2LH-5/pCOS1, CF2LH-6/pCOS1 and CF2LH-7/pCOS1 were prepared.

As a typical example of these plasmids, the construction of the plasmid CF2LH-0/pCOS1 is illustrated in FIG. 37 and the nucleotide sequence and the amino acid sequence of MABL2-scFv <LH-0> contained in the plasmid are shown in SEQ ID No. 54. Nucleotide sequences and amino acid sequences of the linker regions in these plasmids are also shown in FIG. 38. The corresponding amino acid sequence is shown in SEQ ID NO. 103.

6.3 Expression of scFvs and sc(Fv)₂ in COS7 Cells

(1) Preparation of Culture Supernatant Using Serum-Containing Culture Medium

The HL type and LH type of scFvs and sc(FV)₂ were transiently expressed in COS7 cells (JCRB9127, Japan Health Sciences Foundation). COS7 cells were subcultured in

DMEM media (GIBCO BRL) containing 10% fetal bovine serum (HyClone) at 37° C. in carbon dioxide atmosphere incubator. The COS7 cells were transfected with CF2HL-0, 3~7/pCOS1, or CF2LH-0, 3~7/pCOS1 prepared in Example 6.2 or pCHOM2(Fv)₂ vectors by electroporation using the Gene Pulser apparatus (BioRad). The DNA (10 µg) and 0.25 ml of 2×10⁷ cells/ml in DMEM culture medium containing 10% FBS and 5 mM BES (SIGMA) were added to a cuvette. After standing for 10 minutes the mixtures were treated with pulse at 0.17 kV, 950 µF of electric capacity. After the restoration for 10 minutes at room temperature, the electroporated cells were transferred into the DMEM culture medium (10% FBS) in 75 cm³ flask. After culturing for 72 hours, the culture supernatant was collected and centrifuged to remove cell fragments. The culture supernatant was subjected to the filtration using 0.22 µm bottle top filter (FALCON) to obtain the culture supernatant (hereinafter "CM").

(2) Preparation of Culture Supernatant Using Serum-Free Culture Medium

Cells transfected in the same manner as (1) were transferred to the DMEM medium (10% FBS) in 75 cm³ flask and cultured overnight. After the culture, the supernatant was discarded and the cells were washed with PBS and then added to CHO-S-SFM II medium (GIBCO BRL). After culturing for 72 hours, the culture supernatant was collected, centrifuged to remove cell fragments and filtered using 0.22 µm bottle top filter (FALCON) to obtain CM.

6.4 Detection of scFvs and sc(Fv)₂ in CM of COS7

The various MABL2-scFVs and sc(Fv)₂ in CM of COS7 prepared in the aforementioned Example 6.3 (2) were detected by Western Blotting method.

Each CM of COS7 was subjected to SDS-PAGE electrophoresis and transferred to REINFORCED NC membrane (Schleicher & Schuell). The membrane was blocked with 5% skim milk (Morinaga Nyu-gyo) and washed with TBS. Then an anti-FLAG antibody (SIGMA) was added thereto. The membrane was incubated at room temperature and washed. A peroxidase labeled mouse IgG antibody (Jackson Immuno Research) was added. After incubating and washing at room temperature, the substrate solution (Kirkegaard Perry Laboratories) was added to develop color (FIG. 39).

6.5 Flow Cytometry

Flow cytometry was performed using the culture supernatants of COS7 cells prepared in Example 6.3 (1) to measure the binding of the MABL2-scFVs and sc(Fv)₂ to human Integrin Associated Protein (IAP) antigen. The culture supernatants to be tested or a culture supernatant of COS7 cells as a control was added to 2×10⁵ cells of the mouse leukemia cell line L1210 expressing human IAP. After incubating on ice and washing, 10 µg/mL of the mouse anti-FLAG antibody (SIGMA) was added and then the cells were incubated and washed. Then, the FITC labeled anti-mouse IgG antibody (BECTON DICKINSON) was added thereto and the cells were incubated and washed again. The fluorescence intensity was measured using the FACScan apparatus (BECTON DICKINSON). The results of the flow cytometry show that the MABL2-scFvs having linkers with different length and the sc(Fv)₂ in the culture supernatants of COS7 have high affinity to human IAP (see FIGS. 40a and 40b).

6.6 Apoptosis-Inducing Effect in Vitro

An apoptosis-inducing action of the culture supernatants of COS7 prepared in Example 6.3 (1) was examined by Annexin-V staining (Boehringer Mannheim) using the L1210 cells transfected with human IAP gene (hIAP/L1210).

To 5×10⁴ cells of the hIAP/L1210 cells were added the culture supernatants of COS7 cells transfected with each vectors or a culture supernatant of COS7 cells as a control at 10% of the final concentration and the mixtures were cultured for 24 hours. Then, the Annexin-V/PI staining was performed and the fluorescence intensity was measured using the FAC-Scan apparatus (BECTON DICKINSON). The results revealed that scFvs <HL3, 4, 6, 7, LH3, 4, 6, 7> and sc(Fv)₂ in CM of COS7 induced remarkable cell death of hIAP/L1210 cells. These results are shown in FIG. 41.

6.7 Construction of Vectors for the Expression of scFvs and sc(Fv)₂ in CHO Cells

To isolate and purify MABL2-scFvs and sc(Fv)₂ from culture supernatant, the expression vectors for expressing in CHO cells were constructed as below.

The EcoRI-BamHI fragments of pCF2HL-0, 3~7, and pCF2LH-0, 3~7 prepared in Example 6.2 were introduced between EcoRI and BamHI sites in an expression vector pCHO1 for CHO cells using the Ligation High. Competent *E. coli* DH5α was transformed with them. The plasmids were isolated from the transformed *E. coli* using QIAGEN Plasmid Midi kit (QIAGEN) to prepare expression plasmids pCHOM2HL-0, 3~7, and pCHOM2LH-0, 3~7.

6.8 Production of CHO Cells Expressing MABL2-scFvs <HL-0, 3~7>, MABL2-scFvs <LH-0, 3~7> and sc(Fv)₂ and Preparation of the Culture Supernatants Thereof

CHO cells were transfected with each of the expression plasmids pCHOM2HL-0, 3~7, and pCHOM2LH-0, 3~7, constructed in Example 6.7 and pCHOM2(Fv)₂ vector to prepare the CHO cells constantly expressing each reconstructed polypeptide. As a typical example thereof, the production of the CHO cells constantly expressing MABL2-scFv <HL-5> or sc(Fv)₂ is illustrated as follows.

The expression plasmids pCHOM2HL-5 and pCHOM2(Fv)₂ were linearized by digesting with a restriction enzyme PvuI and subjected to transfection to CHO cells by electroporation using Gene Pulser apparatus (BioRad). The DNA (10 µg) and 0.75 ml of PBS with 1×10⁷ cells/ml were added to a cuvette and treated with pulse at 1.5 kV, 25 µF of electric capacity. After the restoration for 10 minutes at room temperature, the electroporated cells were transferred into nucleic acid-containing α-MEM culture medium (GIBCO BRL) containing 10% fetal bovine serum and cultured. After culturing overnight, the supernatant was discarded. The cells were washed with PBS and added to nucleic acid-free α-MEM culture medium (GIBCO BRL) containing 10% fetal bovine serum. After culturing for two weeks, the cells were cultured in a medium containing 10 nM (final concentration) methotrexate (SIGMA), then 50 nM and 100 nM methotrexate. The resultant cells were cultured in serum-free CHO-S-SFM II medium (GIBCO BRL) in a roller bottle. The culture supernatant was collected, centrifuged to remove cell fragments and filtered using a filter with 0.22 µm of pore size to obtain CM, respectively.

According to the above, CHO cells which constantly express MABL2-scFvs <HL-0, -3, -4, -6, -7> and <LH-0, -3, -4, -5, -6, -7> and CMs thereof were obtained.

6.9 Purification of Dimer of MABL2-scFv <HL-5> and sc(Fv)₂

The MABL2-scFv <HL-5> and the sc(Fv)₂ were purified from CMs prepared in Example 6.8 by two types of purification method as below.

<Purification Method 1>

HL-5 and sc(Fv)₂ were purified by the anti-FLAG antibody affinity column chromatography utilizing the FLAG

sequence located at C-terminal of the polypeptides and by gel filtration. One liter of CM as obtained in 6.8 was applied onto a column (7.9 ml) prepared with anti-FLAG M2 Affinity gel (SIGMA) equilibrated with 50 mM Tris-HCl buffer (TBS, pH 7.5) containing 150 mM NaCl. After washing the column with TBS, the scFv was eluted by 0.1 M glycine-HCl buffer, pH 3.5. The resultant fractions were analyzed by SDS-PAGE and the elution of the scFv was confirmed. The scFv fraction was mixed with Tween 20 up to 0.01% of the final concentration and concentrated using Centricon-10 (MILIPORE). The concentrate was applied onto TSKgel G3000SWG column (7.5x600 mm) equilibrated with 20 mM acetate buffer (pH 6.0) containing 150 mM NaCl and 0.01% Tween 20. At 0.4 mL/minute of the flow rate, the scFv was detected by the absorption at 280 nm. The HL-5 was eluted as the major fraction in the position of the dimer and the sc(Fv)₂ was eluted in the position of the monomer.

<Purification Method 2>

HL-5 and sc(Fv)₂ were purified using three steps comprising ion exchange chromatography, hydroxyapatite and gel filtration. In the ion exchange chromatography, Q sepharose fast flow column (Pharmacia) was employed for HL-5 and SP-sepharose fast flow column was employed for sc(Fv)₂. In and after the second step, HL-5 and sc(Fv)₂ were processed by the same procedure.

First Step for HL-5

CM of HL-5 was diluted to two times with 20 mM Tris-HCl buffer (pH 9.0) containing 0.02% Tween 20 and then the pH was adjusted to 9.0 with 1 M Tris. The solution was applied onto Q Sepharose fast flow column equilibrated with 20 mM Tris-HCl buffer (pH 8.5) containing 0.02% Tween 20. A polypeptide adsorbed to the column was eluted by a linear gradient of NaCl in the same buffer, from 0.1 to 0.55 M. Monitoring the eluted fractions by SDS-PAGE, the fractions containing HL-5 were collected and subjected to hydroxyapatite of the second step.

First Step for sc(Fv)₂

CM of the sc(Fv)₂ was diluted to two times with 20 mM acetate buffer (pH 5.5) containing 0.02% Tween 20 and its pH was adjusted to 5.5 with 1 M acetic acid. The solution was applied onto a SP-Sepharose fast flow column equilibrated with 20 mM acetate buffer (pH 5.5) containing 0.02% Tween 20. A polypeptide adsorbed to the column was eluted by a linear gradient of NaCl in the buffer, from 0 to 0.5 M. Monitoring the eluted fractions by SDS-PAGE, the fractions containing the Sc(Fv)₂ were collected and subjected to hydroxyapatite of the second step.

Second Step: Hydroxyapatite Chromatography of HL-5 and sc(Fv)₂

The fractions of HL-5 and sc(Fv)₂ obtained in the first step were separately applied onto the hydroxyapatite column (Type I, BIORAD) equilibrated with 10 mM phosphate buffer containing 0.02% Tween 20, pH 7.0. After washing the column with the same buffer, polypeptides adsorbed to the column were eluted by a linear gradient of the phosphate buffer up to 0.5 M. Monitoring the eluted fractions by SDS-PAGE, the fractions containing the desired polypeptides were collected.

Third Step: Gel Filtration of HL-5 and sc(Fv)₂

Each fraction obtained at the second step was separately concentrated with CentriPrep-10 (MILIPORE) and applied onto a Superdex 200 column (2.6x60 cm, Pharmacia) equilibrated with 20 mM acetate buffer (pH 6.0) containing 0.02% Tween 20 and 0.15 M NaCl. HL-5 was eluted in the position

of the dimer, and sc(Fv)HL-5 and sc(Fv)₂ were eluted in the position of the monomer as a major peak respectively.

Since the monomer of HL-5 was hardly detected by both purification methods, it is proved that the dimers of single-chain Fvs are formed in high yields when the linker for the single-chain Fv contains around 5 amino acids. Furthermore, the dimer of HL-5 and the sc(Fv)₂ were stably preserved for a month at 4° C. after the purification.

6.10 Evaluation of the Binding Activity of Purified Dimer of scFv <HL-5> and sc(Fv)₂ Against Antigen

Flow cytometry was performed using the purified dimer of MABL2-scFv <HL-5> and the purified sc(Fv)₂ in order to evaluate the binding to human Integrin Associated Protein (IAP) antigen. 10 g/ml of the purified dimer of MABL2-scFv <HL-5>, the purified sc(Fv)₂, the antibody MABL-2 as a positive control or a mouse IgG (Zymed) as a negative control was added to 2x10⁵ cells of the mouse leukemia cell line L1210 expressing human IAP (hIAP/L1210) or the cell line L1210 transformed with pCOS1 (pCOS1/L1210) as a control. After incubating on ice and washing, 10 g/mL of the mouse anti-FLAG antibody (SIGMA) was added and then the cells were incubated and washed. FITC labeled anti-mouse IgG antibody (BECTON DICKINSON) was added thereto and the cells were incubated and washed again. Then the fluorescence intensity was measured using the FACScan apparatus (BECTON DICKINSON).

Since the purified dimer of MABL2-scFv <HL-5> and the purified sc(Fv)₂ were specifically bound to hIAP/L1210 cells, it is confirmed that the dimer of scFv <HL-5> and the sc(Fv)₂ have high affinity to human IAP (see FIG. 42).

6.11 Apoptosis-Inducing Activity in Vitro of Purified Dimer of scFv <HL-5> and sc(Fv)₂

An apoptosis-inducing action of the purified dimer of MABL2-scFv <HL-5> and the purified sc(Fv)₂ were examined by Annexin-V staining (Boehringer Mannheim) using the L1210 cells (hIAP/L1210) in which human IAP gene had been introduced and cells of human leukemic cell line CCRF-CEM.

Different concentrations of the purified dimer of MABL2-scFv <HL-5>, the purified MABL2-sc(Fv)₂, the antibody MABL-2 as a positive control or a mouse IgG as a negative control were added to 5x10⁴ cells of hIAP/L1210 cell line or 1x10⁵ cells of CCRF-CEM cell line. After culturing for 24 hours, the Annexin-V staining was carried out and the fluorescence intensity thereof was measured using the FACScan apparatus (BECTON DICKINSON). As a result the dimer of MABL2-scFv <HL-5> and the MABL2-sc(Fv)₂ remarkably induced cell death of hIAP/L1210 and CCRF-CEM in concentration-dependent manner (see FIG. 43).

6.12 Hemagglutination Test of the Purified Dimer of scFv <HL-5> and the sc(Fv)₂

Hemagglutination test was carried out using different concentrations of the purified dimer of scFv <HL-5> and the purified sc(Fv)₂ in accordance with Example 5.15.

The hemagglutination was observed with the antibody MABL-2 as a positive control, whereas no hemagglutination was observed with both the single chain antibody MABL2-sc(Fv)₂ and the MABL2-scFv <HL-5>. Further, there was no substantial difference in the hemagglutination between two buffers employed with the antibody MABL-2. These results are shown in Table 3.

TABLE 3

H magglutination Test																
Diluent:PBS	cont	28.9	14.45	7.225	3.6125	1.8063	0.9031	0.4516	0.2258	0.1129	0.0564	0.0282	0.0141	0.0071	0.0035	($\mu\text{g/ml}$) 0.0018
MA-BL2-sc (Fv) ₂	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
cont	28.0	14.0	7.0	3.5	1.75	0.875	0.4375	0.2188	0.1094	0.0547	0.0273	0.0137	0.0068	0.0034	0.0017	
MA-BL2-sc (Fv) <HL-5>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
cont	80	40	20	10	5	2.5	1.25	0.625	0.3125	0.1563	0.0781	0.0391	0.0195	0.0098	0.0049	
MA-BL2-(in-tact) mlgG	-	+	+	+	+	+	+	+	+	±	-	-	-	-	-	-
Diluent:Acetate	cont	80	40	20	10	5	2.5	1.25	0.625	0.3125	0.1563	0.0781	0.0391	0.0195	0.0098	($\mu\text{g/ml}$) 0.0049
MA-BL2-(in-tact)	-	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-

6.13 Antitumor Effect of the Purified Dimer of scFv <HL-5> and the sc(Fv)₂ for a Model Mouse of Human Myeloma

The antitumor effects were tested for the dimer of scFv <HL-5> and the sc(Fv)₂ prepared and purified in Examples 6.8 and 6.9. The test was performed by using the mouse model for human myeloma produced in Example 5.1 and determining the amount of M protein produced by human myeloma cells in the mouse serum using ELISA and examine survival time of the mice. Then, the antitumor effects of the dimer of scFv <HL-5> and the sc(Fv)₂ were evaluated in terms of the change of the amount of M protein in the mouse serum and the survival time of the mice.

In the test, the HL-5 and the sc(Fv)₂ were employed as a solution at 0.01, 0.1 or 1 mg/mL in vehicle consisting of 150 mM NaCl, 0.02% Tween and 20 mM acetate buffer, pH 6.0 and administered to the mice at 0.1, 1 or 10 mg/kg of dosage. Control group of mice were administered only with the vehicle.

The mouse serum was gathered 26 days after the transplantation of the human myeloma cells and the amount of M protein in the serum was measured using ELISA according to Example 5.14. As a result, the amount of M protein in the serum of both mice groups administered with HL-5, the dimer and the sc(Fv)₂ decreased in dose-dependent manner (see FIG. 44). Furthermore, a significant elongation of the survival time was observed in both groups administered with the HL-5 (FIG. 45) and with the sc(Fv)₂ (FIG. 46) in comparison with the control group administered with the vehicle. These results show that the HL-5 and the sc(Fv)₂ of the invention have excellent antitumor effect in vivo.

EXPLANATION OF DRAWINGS

FIG. 1 shows the result of flow cytometry, illustrating that human IgG antibody does not bind to L1210 cells expressing human IAP (hIAP/L1210).

FIG. 2 shows the result of flow cytometry, illustrating that the chimera MABL-1 antibody specifically binds to L1210 cells expressing human IAP (hIAP/L1210).

FIG. 3 shows the result of flow cytometry, illustrating that the chimera MABL-2 antibody specifically binds to L1210 cells expressing human IAP (hIAP/L1210).

FIG. 4 schematically illustrates the process for producing the single-chain Fv according to the present invention.

FIG. 5 illustrates a structure of an expression plasmid which can be used to express a DNA encoding the single-chain Fv of the invention in *E. coli*. The (Gly₄Ser)₃ linker is shown in SEQ ID NO: 19.

FIG. 6 illustrates a structure of an expression plasmid which is used to express a DNA encoding the single-chain Fv of the invention in mammalian cells. The (Gly₄Ser)₃ linker is shown in SEQ ID NO: 19.

FIG. 7 shows a photograph showing the result of western blotting in Example 5.4. From the left, a molecular weight marker (which indicates 97.4, 66, 45, 31, 21.5 and 14.5 kDa from the top), the culture supernatant of pCHO1-introduced COS7 cells and the culture supernatant of pCHOM2-introduced COS7 cells. It illustrates that the reconstructed single-chain Fv of the antibody MABL-2 (arrow) is contained in the culture supernatant of the pCHOM2-introduced cells.

FIG. 8 shows the result of flow cytometry, illustrating that an antibody in the culture supernatant of pCHO1/COS7 cell as a control does not bind to pCOS1/L1210 cell as a control.

FIG. 9 shows the result of flow cytometry, illustrating that an antibody in the culture supernatant of MABL2-scFv/COS7 cells does not bind to pCOS1/L1210 cells as a control.

FIG. 10 shows the result of flow cytometry, illustrating that an antibody in the culture supernatant of pCOS1/COS7 cells as a control does not bind to hIAP/L1210 cells.

FIG. 11 shows the result of flow cytometry, illustrating that an antibody in the culture supernatant of MABL2-scFv/COS7 cells specifically binds to hIAP/L1210 cells.

FIG. 12 shows the result of the competitive ELISA in Example 5.6, wherein the binding activity of the single-chain Fv of the invention (MABL2-scFv) to the antigen is demonstrated in terms of the inhibition of binding of the mouse monoclonal antibody MABL-2 to the antigen as an index, in comparison with the culture supernatant of pCHO1/COS7 cells as a control.

FIG. 13 shows the results of the apoptosis-inducing effect in Example 5.7, illustrating that the antibody in the culture supernatant of pCHO1/COS7 cells as a control does not induce the apoptosis of pCOS1/L1210 cells as a control.

FIG. 14 shows the results of the apoptosis-inducing effect in Example 5.7, illustrating that the antibody in the culture supernatant of MABL2-scFv/COS7 cells does not induce apoptosis of pCOS1/L1210 cells as a control.

FIG. 15 shows the results of the apoptosis-inducing effect in Example 5.7, illustrating that the antibody in the culture supernatant of pCHO1/COS7 cells as a control does not induce apoptosis of hIAP/L1210 cells.

FIG. 16 shows the results of the apoptosis-inducing effect in Example 5.7, illustrating that the antibody in the culture supernatant of MABL2-scFv/COS7 cells specifically induces apoptosis of hIAP/L1210 cells.

FIG. 17 shows the results of the apoptosis-inducing effect in Example 5.7, illustrating that the antibody in the culture supernatant of pCHO1/COS7 cells as a control does not induce apoptosis of CCRF-CEM cells (at 50% of the final concentration).

FIG. 18 shows the results of the apoptosis-inducing effect in Example 5.7, illustrating that the antibody in the culture supernatant of MABL2-scFv/COS7 cells specifically induces apoptosis of CCRF-CEM cells (at 50% of the final concentration).

FIG. 19 shows the chromatogram obtained in the purification of the single-chain Fv derived from the antibody MABL-2 produced by the CHO cells in Example 5.9, illustrating that fraction A and fraction B were obtained as the major peaks when the fraction from Blue-sepharose column was purified with hydroxyapatite column.

FIG. 20 shows the results of purification by gel filtration of fraction A and fraction B obtained in Example 5.9-(2), illustrating that the major peaks (AI and BI, respectively) were eluted from fraction A at approximately 36 kD of the apparent molecular weight and from fraction B at approximately 76 kD.

FIG. 21 is the analysis on SDS-PAGE of the fractions obtained in the purification of the single chain Fv derived from the antibody MABL-2 produced by the CHO cells in Example 5.9, illustrating that a single band of approximately 35 kD of molecular weight was observed in both fractions.

FIG. 22 shows the results of analysis of fractions AI and BI obtained by gel filtration in the purification of the single-chain Fv derived from the antibody MABL-2 produced by the CHO cells, wherein fraction AI comprises monomer and fraction BI comprises dimer.

FIG. 23 illustrates a structure of an expression plasmid which can be used to express a DNA encoding the single-chain Fv of the invention in *E. coli*. The $(\text{Gly}_4\text{Ser})_3$ linker is shown in SEQ ID NO: 19.

FIG. 24 shows the results of purification on the gel filtration column of crude products of the single-chain Fv polypeptide derived from the antibody MABL-2 produced by *E. coli* obtained in Example 5.12, wherein each peak indicates monomer or dimer, respectively, of the single-chain Fv produced by *E. coli*.

FIG. 25 shows the results of the apoptosis-inducing effect in Example 5.13, illustrating that mouse IgG antibody as a control does not induce apoptosis of hIAP/L1210 cells (the final concentration of 3 $\mu\text{g/ml}$).

FIG. 26 shows the results of the apoptosis-inducing effect in Example 5.13, illustrating that the dimer of MABL2-scFv produced by the CHO cells remarkably induces apoptosis of hIAP/L1210 cells (the final concentration of 3 $\mu\text{g/ml}$).

FIG. 27 shows the results of the apoptosis-inducing effect in Example 5.13, illustrating that the dimer of MABL2-scFv produced by *E. coli* remarkably induces apoptosis of hIAP/L1210 cells (the final concentration of 3 $\mu\text{g/ml}$).

FIG. 28 shows the results of the apoptosis-inducing effect in Example 5.13, illustrating that apoptosis induction to hIAP/L1210 cells by the MABL2-scFv monomer produced by the CHO cells is the same level as that of the control (the final concentration of 3 $\mu\text{g/ml}$).

FIG. 29 shows the results of the apoptosis-inducing effect in Example 5.13, illustrating that apoptosis induction to hIAP/L1210 cells of the MABL2-scFv monomer produced by *E. coli* is the same level as that of control (the final concentration of 3 $\mu\text{g/ml}$).

FIG. 30 shows the results of the apoptosis-inducing effect in Example 5.13, illustrating that mouse IgG antibody used as a control does not induce apoptosis of hIAP/L1210 cells even when anti-FLAG antibody is added (the final concentration of 3 $\mu\text{g/ml}$).

FIG. 31 shows the results of the apoptosis-inducing effect in Example 5.13, illustrating that MABL2-scFv monomer produced by the CHO cells remarkably induces apoptosis of hIAP/L1210 cells when anti-FLAG antibody is added (the final concentration of 3 $\mu\text{g/ml}$).

FIG. 32 shows the results of quantitative measurement of human IgG in the serum of a human myeloma cell line KPMM2-transplanted mouse, indicating amounts of human IgG produced by the human myeloma cells in the mouse. It illustrates that the dimer of scFv/CHO remarkably inhibited growth of the KPMM2 cells.

FIG. 33 shows the survival time of the mouse after the transplantation of tumor, illustrating that the scFv/CHO dimer-administered group elongated remarkably the survival time.

FIG. 34 illustrates a structure of an expression plasmid which expresses a reconstructed polypeptide comprising two H chain V regions and two L chain V regions derived from the antibody MABL-2. The $(\text{Gly}_4\text{Ser})_3$ linker is shown in SEQ ID NO: 19 and the $(\text{Gly}_4\text{Ser})_3\text{VSD}$ linker is shown in SEQ ID NO: 55.

FIG. 35 illustrates a structure of a plasmid which expresses a scFv (HL type) wherein the V regions are linked in the manner of [H chain]-[L chain] without a peptide linker.

FIG. 36 illustrates a structure of the HL-type nucleotide (SEQ ID NOS 56, 58, 60, 62, 64 and 66, respectively, in order of appearance) and amino acid sequences (SEQ ID NOS 57, 59, 61, 63, 65 and 67, respectively, in order of appearance) of peptide linkers.

FIG. 37 illustrates a structure of a plasmid which expresses a scFv (LH type) wherein the V regions are linked in the manner of [L chain]-[H chain] without a peptide linker.

FIG. 38 illustrates a structure of the LH-type nucleotide (SEQ ID NOS 68, 70, 72, 74, 76 and 78, respectively, in order of appearance) and amino acid sequences (SEQ ID NOS 69, 71, 73, 75, 77 and 79, respectively, in order of appearance) of peptide linkers.

FIG. 39 shows the results of the western blotting in Example 6.4, illustrating that the reconstructed polypeptide sc(Fv)₂ comprising two H chain V regions and two L chain V regions, and the MABL2-scFv having peptide linkers with different length are expressed.

FIGS. 40a and 40b show the results of flow cytometry using the culture supernatant of COS7 cells prepared in Example 6.3 (1), illustrating that the MABL2-scFv and sc(Fv)₂ having peptide linkers with different length have high affinities against human IAP.

FIG. 41 shows the results of the apoptosis-inducing effect in Example 6.6, illustrating that the scFv <HL3, 4, 6, 7, LH3, 4, 6 and 7> and the sc(Fv)₂ remarkably induce cell death of hIAP/L1210 cells.

FIG. 42 shows the results of the evaluation of antigen binding capacity in Example 6.10, illustrating that the dimer of scFv <HL5> and sc(Fv)₂ have high affinities against human IAP.

FIG. 43 shows the results of the in vitro apoptosis-inducing effect in Example 6.11, illustrating that the dimer of scFv

<HL5> and the sc(Fv)₂ induce apoptosis of hIAP/L1210 cells and CCRF-CEM cells in concentration-dependent manner.

FIG. 44 shows the results of the quantitative measurement of M protein produced by a human myeloma cell line KPMM2 in the serum of the human myeloma cell-transplanted mouse. It illustrates that the dimer of scFv <HL5> and the sc(Fv)₂ remarkably inhibited growth of the KPMM2 cells.

FIG. 45 shows the survival time (days) of mice after the transplantation of tumor, illustrating that the survival time of the scFv <HL5> administrated-group was remarkably prolonged.

FIG. 46 shows the survival time (days) of mice after the transplantation of tumor, illustrating that the survival time of the sc(Fv)₂ administrated-group was remarkably prolonged.

INDUSTRIAL APPLICABILITY

The reconstructed polypeptides of the invention have properties of inducing apoptosis of nucleated blood cells having Integrin Associated Protein (IAP) and causing no hemagglutination, and are useful as a therapeutic agent for blood dyscrasia, for example, leukemia such as acute myeloid leukemia, chronic myelogenous leukemia, acute lymphoblastic leukemia, chronic lymphocytic leukemia, adult T-cell leukemia, multiple myeloma, mixed leukemia and hairy cell leukemia, malignant lymphoma (Hodgkin's disease, non-Hodgkin's lymphoma), aplastic anemia, myelodysplasia syndrome and polycythemia vera.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 103

<210> SEQ ID NO 1

<211> LENGTH: 27

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 1

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27

<210> SEQ ID NO 2

<211> LENGTH: 27

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 2

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27

<210> SEQ ID NO 3

<211> LENGTH: 28

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 3

ggatcccggg ccagtggata gacagatg

28

<210> SEQ ID NO 4

<211> LENGTH: 26

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 4

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<210> SEQ ID NO 5
<211> LENGTH: 394
<212> TYPE: DNA
<213> ORGANISM: Mus sp.
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(393)
<223> OTHER INFORMATION: pGEM-M1L
<220> FEATURE:
<221> NAME/KEY: sig_peptide
<222> LOCATION: (1)..(57)
<220> FEATURE:
<221> NAME/KEY: mat_peptide
<222> LOCATION: (58)..(393)

<400> SEQUENCE: 5

atg aag ttg cct gtt agg ctg ttg gtg ctg atg ttc tgg att cct gcg       48
Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
      -15                    -10                    -5

tcc agc agt gat gtt gtg atg acc caa act cca ctc tcc ctg cct gtc       96
Ser Ser Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val
      -1  1                    5                    10

agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt cag agc ctt      144
Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
      15                    20                    25

cta cac agt aaa gga aac acc tat tta caa tgg tac cta cag aag cca      192
Leu His Ser Lys Gly Asn Thr Tyr Leu Gln Trp Tyr Leu Gln Lys Pro
      30                    35                    40                    45

ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt tct      240
Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
      50                    55                    60

ggg gtc cca gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca      288
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
      65                    70                    75

ctc aag atc agc aga gtg gag gct gag gat ctg gga gtt tat ttc tgc      336
Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
      80                    85                    90

tct caa agt aca cat gtt ccg tac acg tcc gga ggg ggg acc aag ctg      384
Ser Gln Ser Thr His Val Pro Tyr Thr Ser Gly Gly Gly Thr Lys Leu
      95                    100                    105

gaa ata aaa c                                               394
Glu Ile Lys
110

<210> SEQ ID NO 6
<211> LENGTH: 409
<212> TYPE: DNA
<213> ORGANISM: Mus sp.
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(408)
<223> OTHER INFORMATION: pGEM-M1H
<220> FEATURE:
<221> NAME/KEY: sig_peptide
<222> LOCATION: (1)..(57)
<220> FEATURE:
<221> NAME/KEY: mat_peptide
<222> LOCATION: (58)..(408)

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<400> SEQUENCE: 6

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atg gaa tgg agc tgg ata ttt ctc ttc ctg tca gga act gca ggt      48
Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
      -15                      -10                      -5

gtc cac tcc cag gtc cag ctg cag cag tct gga cct gac ctg gta aag      96
Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Asp Leu Val Lys
      -1  1                      5                      10

cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga tac acc ttc      144
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
      15                      20                      25

gtt aac cat gtt atg cac tgg gtg aag cag aag cca ggg cag ggc ctt      192
Val Asn His Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
      30                      35                      40                      45

gag tgg att gga tat att tat cct tac aat gat ggt act aag tac aat      240
Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
      50                      55                      60

gag aag ttc aag ggc aag gcc aca ctg act tca gag aaa tcc tcc agc      288
Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Glu Lys Ser Ser Ser
      65                      70                      75

gca gcc tac atg gag ctc agc agc ctg gcc tct gag gac tct gcg gtc      336
Ala Ala Tyr Met Glu Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val
      80                      85                      90

tac tac tgt gca aga ggg ggt tac tat agt tac gac gac tgg ggc caa      384
Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Ser Tyr Asp Asp Trp Gly Gln
      95                      100                      105

ggc acc act ctc aca gtc tcc tca g      409
Gly Thr Thr Leu Thr Val Ser Ser
110                      115

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<210> SEQ ID NO 7

<211> LENGTH: 394

<212> TYPE: DNA

<213> ORGANISM: Mus sp.

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(393)

<223> OTHER INFORMATION: pGEM-M2L

<220> FEATURE:

<221> NAME/KEY: sig_peptide

<222> LOCATION: (1)..(57)

<220> FEATURE:

<221> NAME/KEY: mat_peptide

<222> LOCATION: (58)..(393)

<400> SEQUENCE: 7

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atg aag ttg cct gtt agg ctg ttg gtg ctg atg ttc tgg att cct ggt      48
Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Gly
      -15                      -10                      -5

tcc agc agt gat gtt gtg atg acc caa agt cca ctc tcc ctg cct gtc      96
Ser Ser Ser Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val
      -1  1                      5                      10

agt ctt gga gat caa gcc tcc atc tct tgc aga tca agt cag agc ctt      144
Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
      15                      20                      25

gtg cac agt aat gga aag acc tat tta cat tgg tac ctg cag aag cca      192
Val His Ser Asn Gly Lys Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
      30                      35                      40                      45

ggc cag tct cca aaa ctc ctg atc tac aaa gtt tcc aac cga ttt tct      240
Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
      50                      55                      60

ggg gtc cca gac agg ttc agt ggc agt gga tca gtg aca gat ttc aca      288
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Val Thr Asp Phe Thr
      65                      70                      75

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```
ctc atg atc agc aga gtg gag gct gag gat ctg gga gtt tat ttc tgc      336
Leu Met Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
      80                      85                      90
```

```
tct caa agt aca cat gtt ccg tac acg ttc gga ggg ggg acc aag ctg      384
Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
      95                      100                      105
```

```
gaa ata aaa c      394
Glu Ile Lys
110
```

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<210> SEQ ID NO 8
<211> LENGTH: 409
<212> TYPE: DNA
<213> ORGANISM: Mus sp.
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(408)
<223> OTHER INFORMATION: pGEM-M2H
<220> FEATURE:
<221> NAME/KEY: sig_peptide
<222> LOCATION: (1)..(57)
<220> FEATURE:
<221> NAME/KEY: mat_peptide
<222> LOCATION: (58)..(408)
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<400> SEQUENCE: 8
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```
atg gaa tgg agc tgg ata ttt ctc ttc ctc ctg tca gga act gca ggt      48
Met Glu Trp Ser Trp Ile Phe Leu Leu Ser Gly Thr Ala Gly
      -15                      -10                      -5
```

```
gtc cac tcc cag gtc cag ctg cag cag tct gga cct gaa ctg gta aag      96
Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
      -1  1                      5                      10
```

```
cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga tac acc ttc      144
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
      15                      20                      25
```

```
gct aac cat gtt att cac tgg gtg aag cag aag cca ggg cag ggc ctt      192
Ala Asn His Val Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
      30                      35                      40                      45
```

```
gag tgg att gga tat att tat cct tac aat gat ggt act aag tat aat      240
Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
      50                      55                      60
```

```
gag aag ttc aag gac aag gcc act ctg act tca gac aaa tcc tcc acc      288
Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Thr
      65                      70                      75
```

```
aca gcc tac atg gac ctc agc agc ctg gcc tct gag gac tct gcg gtc      336
Thr Ala Tyr Met Asp Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val
      80                      85                      90
```

```
tat tac tgt gca aga ggg ggt tac tat act tac gac gac tgg ggc caa      384
Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Thr Tyr Asp Asp Trp Gly Gln
      95                      100                      105
```

```
ggc acc act ctc aca gtc tcc tca g      409
Gly Thr Thr Leu Thr Val Ser Ser
110                      115
```

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<210> SEQ ID NO 9
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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<400> SEQUENCE: 9
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cccaagcttc caccatgaag ttgcctgtta gg      32
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<210> SEQ ID NO 10
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 10

cccaagcttc caccatggaa tggagctgga ta 32

<210> SEQ ID NO 11
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 11

cgcgatcca ctcaegtttt atttcagct tggc 34

<210> SEQ ID NO 12
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 12

cgcgatcca ctcaectgag gagactgtga gact 34

<210> SEQ ID NO 13
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 13

catgccatgg cgcaggtcca gctgcagcag 30

<210> SEQ ID NO 14
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 14

accaccacct gaggagactg tgagagt 27

<210> SEQ ID NO 15
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 15

gtctcctcag gtggtggtgg ttcgggt 27

<210> SEQ ID NO 16
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

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<400> SEQUENCE: 16
cacaacatcc gatccgccac caccgga 27

<210> SEQ ID NO 17
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 17
ggcggatcgg atgttgtgat gacccaa 27

<210> SEQ ID NO 18
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 18
ccggaattct cattatttat cgtcatcgtc tttgtagtct tttatttcca gcttggt 57

<210> SEQ ID NO 19
<211> LENGTH: 45
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Linker
nucleotide sequence
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(45)

<400> SEQUENCE: 19
ggt ggt ggt ggt tcg ggt ggt ggt ggt tcg ggt ggt ggc gga tcg 45
Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> SEQ ID NO 20
<211> LENGTH: 828
<212> TYPE: DNA
<213> ORGANISM: Mus sp.
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(822)
<223> OTHER INFORMATION: pscM1. MABL1-scFv

<400> SEQUENCE: 20
atg aaa tac cta ttg cct acg gca gcc gct gga ttg tta tta ctc gct 48
Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1 5 10 15

gcc caa cca gcc atg gcg cag gtc cag ctg cag cag tct gga cct gac 96
Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Gln Ser Gly Pro Asp
20 25 30

ctg gta aag cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga 144
Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
35 40 45

tac acc ttc gtt aac cat gtt atg cac tgg gtg aag cag aag cca ggg 192
Tyr Thr Phe Val Asn His Val Met His Trp Val Lys Gln Lys Pro Gly
50 55 60

cag gcc ctt gag tgg att gga tat att tat cct tac aat gat ggt act 240
Gln Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr
65 70 75 80

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aag tac aat gag aag ttc aag ggc aag gcc aca ctg act tca gag aaa	288
Lys Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Glu Lys	
85 90 95	
tcc tcc agc gca gcc tac atg gag ctc agc agc ctg gcc tct gag gac	336
Ser Ser Ser Ala Ala Tyr Met Glu Leu Ser Ser Leu Ala Ser Glu Asp	
100 105 110	
tct gcg gtc tac tac tgt gca aga ggg ggt tac tat agt tac gac gac	384
Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Ser Tyr Asp Asp	
115 120 125	
tgg gcc caa ggc acc act ctc aca gtc tcc tca ggt ggt ggt ggt tcg	432
Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Ser	
130 135 140	
ggg ggt ggt ggt tcg ggt ggt gcc gga tcg gat gtt gtg atg acc caa	480
Gly Gly Gly Gly Ser Gly Gly Gly Ser Asp Val Val Met Thr Gln	
145 150 155 160	
act cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct	528
Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser	
165 170 175	
tgc aga tct agt cag agc ctt cta cac agt aaa gga aac acc tat tta	576
Cys Arg Ser Ser Gln Ser Leu Leu His Ser Lys Gly Asn Thr Tyr Leu	
180 185 190	
caa tgg tac cta cag aag cca ggc cag tct cca aag ctc ctg atc tac	624
Gln Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr	
195 200 205	
aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt	672
Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser	
210 215 220	
gga tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag	720
Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu	
225 230 235 240	
gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg	768
Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr	
245 250 255	
tcc gga ggg ggg acc aag ctg gaa ata aaa gac tac aaa gac gat gac	816
Ser Gly Gly Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp	
260 265 270	
gat aaa taatga	828
Asp Lys	

<210> SEQ ID NO 21
 <211> LENGTH: 31
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 <400> SEQUENCE: 21

acgcgtcgac tcccagggtcc agctgcagca g 31

<210> SEQ ID NO 22
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 <400> SEQUENCE: 22

gaaggtgtat ccagaagc 18

<210> SEQ ID NO 23
 <211> LENGTH: 819
 <212> TYPE: DNA

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<210> SEQ ID NO 24
<211> LENGTH: 828
<212> TYPE: DNA
<213> ORGANISM: Mus sp.
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(822)
<223> OTHER INFORMATION: pscM2. MABL2-scFv

<400> SEQUENCE: 24

atg aaa tac cta ttg cct acg gca gcc gct gga ttg tta tta ctc gct      48
Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
  1          5          10          15

gcc caa cca gcc atg gcg cag gtc cag ctg cag cag tct gga cct gaa      96
Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Gln Ser Gly Pro Glu
  20          25          30

ctg gta aag cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga      144
Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
  35          40          45

tac acc ttc gct aac cat gtt att cac tgg gtg aag cag aag cca ggg      192
Tyr Thr Phe Ala Asn His Val Ile His Trp Val Lys Gln Lys Pro Gly
  50          55          60

cag gcc ctt gag tgg att gga tat att tat cct tac aat gat ggt act      240
Gln Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr
  65          70          75          80

aag tat aat gag aag ttc aag gac aag gcc act ctg act tca gac aaa      288
Lys Tyr Asn Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr Ser Asp Lys
  85          90          95

tcc tcc acc aca gcc tac atg gac ctc agc agc ctg gcc tct gag gac      336
Ser Ser Thr Thr Ala Tyr Met Asp Leu Ser Ser Leu Ala Ser Glu Asp
  100         105         110

tct gcg gtc tat tac tgt gca aga ggg ggt tac tat act tac gac gac      384
Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Thr Tyr Asp Asp
  115         120         125

tgg gcc caa gcc acc act ctc aca gtc tcc tca ggt ggt ggt ggt tcg      432
Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser
  130         135         140

ggg ggt ggt ggt tcg ggt ggt gcc gga tcg gat gtt gtg atg acc caa      480
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
  145         150         155         160

agt cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct      528
Ser Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser
  165         170         175

tgc aga tca agt cag agc ctt gtg cac agt aat gga aag acc tat tta      576
Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Lys Thr Tyr Leu
  180         185         190

cat tgg tac ctg cag aag cca gcc cag tct cca aaa ctc ctg atc tac      624
His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr
  195         200         205

aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt      672
Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
  210         215         220

gga tca gtg aca gat ttc aca ctc atg atc agc aga gtg gag gct gag      720
Gly Ser Val Thr Asp Phe Thr Leu Met Ile Ser Arg Val Glu Ala Glu
  225         230         235         240

gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg      768
Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr
  245         250         255

ttc gga ggg ggg acc aag ctg gaa ata aaa gac tac aaa gac gat gac      816
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp
  260         265         270

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gat aaa taatga                               828
Asp Lys

<210> SEQ ID NO 25
<211> LENGTH: 819
<212> TYPE: DNA
<213> ORGANISM: Mus sp.
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(813)
<223> OTHER INFORMATION: pCHOM2. MABL2-scFv

<400> SEQUENCE: 25

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt      48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
  1             5             10             15

gtc gac tcc cag gtc cag ctg cag cag tct gga cct gaa ctg gta aag      96
Val Asp Ser Gln Val Gln Leu Gln Ser Gly Pro Glu Leu Val Lys
             20             25             30

cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga tac acc ttc     144
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
             35             40             45

gct aac cat gtt att cac tgg gtg aag cag aag cca ggg cag ggc ctt     192
Ala Asn His Val Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
  50             55             60

gag tgg att gga tat att tat cct tac aat gat ggt act aag tat aat     240
Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
  65             70             75             80

gag aag ttc aag gac aag gcc act ctg act tca gac aaa tcc tcc acc     288
Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Thr
             85             90             95

aca gcc tac atg gac ctc agc agc ctg gcc tct gag gac tct gcg gtc     336
Thr Ala Tyr Met Asp Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val
             100            105            110

tat tac tgt gca aga ggg ggt tac tat act tac gac gac tgg ggc caa     384
Tyr Tyr Cys Ala Arg Gly Gly Tyr Thr Tyr Asp Asp Trp Gly Gln
             115            120            125

ggc acc act ctc aca gtc tcc tca ggt ggt ggt ggt tcc ggt ggt ggt     432
Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
             130            135            140

ggt tcc ggt ggt ggc gga tcc gat gtt gtg atg acc caa agt cca ctc     480
Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser Pro Leu
             145            150            155            160

tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tca     528
Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser
             165            170            175

agt cag agc ctt gtg cac agt aat gga aag acc tat tta cat tgg tac     576
Ser Gln Ser Leu Val His Ser Asn Gly Lys Thr Tyr Leu His Trp Tyr
             180            185            190

ctg cag aag cca ggc cag tct cca aaa ctc ctg atc tac aaa gtt tcc     624
Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser
             195            200            205

aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca gtg     672
Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Val
             210            215            220

aca gat ttc aca ctc atg atc agc aga gtg gag gct gag gat ctg gga     720
Thr Asp Phe Thr Leu Met Ile Ser Arg Val Glu Ala Glu Asp Leu Gly
             225            230            235            240

ggt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc gga ggg     768
Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly
             245            250            255

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ggg acc aag ctg gaa ata aaa gac tac aaa gac gat gac gat aaa      813
Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp Asp Lys
                260                      265                      270

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taatga                                                                819

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```

<210> SEQ ID NO 26
<211> LENGTH: 456
<212> TYPE: DNA
<213> ORGANISM: Mus sp.
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(450)
<223> OTHER INFORMATION: pCHO-shIAP. Soluble human IAP

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<400> SEQUENCE: 26

```

```

atg tgg ccc ctg gta gcg gcg ctg ttg ctg ggc tcg gcg tgc tgc gga      48
Met Trp Pro Leu Val Ala Ala Leu Leu Leu Gly Ser Ala Cys Cys Gly
  1                5                10                15

```

```

tca gct cag cta cta ttt aat aaa aca aaa tct gta gaa ttc acg ttt      96
Ser Ala Gln Leu Leu Phe Asn Lys Thr Lys Ser Val Glu Phe Thr Phe
                20                25                30

```

```

tgt aat gac act gtc gtc att cca tgc ttt gtt act aat atg gag gca      144
Cys Asn Asp Thr Val Val Ile Pro Cys Phe Val Thr Asn Met Glu Ala
  35                40                45

```

```

caa aac act act gaa gta tac gta aag tgg aaa ttt aaa gga aga gat      192
Gln Asn Thr Thr Glu Val Tyr Val Lys Trp Lys Phe Lys Gly Arg Asp
  50                55                60

```

```

att tac acc ttt gat gga gct cta aac aag tcc act gtc ccc act gac      240
Ile Tyr Thr Phe Asp Gly Ala Leu Asn Lys Ser Thr Val Pro Thr Asp
  65                70                75                80

```

```

ttt agt agt gca aaa att gaa gtc tca caa tta cta aaa gga gat gcc      288
Phe Ser Ser Ala Lys Ile Glu Val Ser Gln Leu Leu Lys Gly Asp Ala
                85                90                95

```

```

tct ttg aag atg gat aag agt gat gct gtc tca cac aca gga aac tac      336
Ser Leu Lys Met Asp Lys Ser Asp Ala Val Ser His Thr Gly Asn Tyr
  100                105                110

```

```

act tgt gaa gta aca gaa tta acc aga gaa ggt gaa acg atc atc gag      384
Thr Cys Glu Val Thr Glu Leu Thr Arg Glu Gly Glu Thr Ile Ile Glu
  115                120                125

```

```

cta aaa tat cgt gtt gtt tca tgg ttt tct cca aat gaa aat gac tac      432
Leu Lys Tyr Arg Val Val Ser Trp Phe Ser Pro Asn Glu Asn Asp Tyr
  130                135                140

```

```

aag gac gac gat gac aag tgatag                                     456
Lys Asp Asp Asp Asp Lys
  145                150

```

```

<210> SEQ ID NO 27
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

```

```

<400> SEQUENCE: 27

```

```

ggaattccat atgcaagtgc aacttcaaca gtctggacct gaactg                                     46

```

```

<210> SEQ ID NO 28
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

```

```

<400> SEQUENCE: 28

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ggaattctca ttattttatt tccagcttgg t 31

<210> SEQ ID NO 29
 <211> LENGTH: 741
 <212> TYPE: DNA
 <213> ORGANISM: Mus sp.
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(735)
 <223> OTHER INFORMATION: pscM2DEm02. MABL2-scFv

<400> SEQUENCE: 29

atg caa gtg caa ctt caa cag tct gga cct gaa ctg gta aag cct ggg 48
 Met Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly
 1 5 10 15

gct tca gtg aag atg tcc tgc aag gct tct gga tac acc ttc gct aac 96
 Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Asn
 20 25 30

cat gtt att cac tgg gtg aag cag aag cca ggg cag ggc ctt gag tgg 144
 His Val Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp
 35 40 45

att gga tat att tat cct tac aat gat ggt act aag tat aat gag aag 192
 Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys
 50 55 60

ttc aag gac aag gcc act ctg act tca gac aaa tcc tcc acc aca gcc 240
 Phe Lys Asp Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Thr Thr Ala
 65 70 75 80

tac atg gac ctc agc agc ctg gcc tct gag gac tct gcg gtc tat tac 288
 Tyr Met Asp Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Tyr
 85 90 95

tgt gca aga ggg ggt tac tat act tac gac gac tgg ggc caa ggc acc 336
 Cys Ala Arg Gly Gly Tyr Tyr Thr Tyr Asp Asp Trp Gly Gln Gly Thr
 100 105 110

act ctc aca gtc tcc tca ggt ggt ggt ggt tgg ggt ggt ggt tgg 384
 Thr Leu Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser
 115 120 125

ggg ggt ggc gga tgg gat gtt gtg atg acc caa agt cca ctc tcc ctg 432
 Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu
 130 135 140

cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tca agt cag 480
 Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
 145 150 155 160

agc ctt gtg cac agt aat gga aag acc tat tta cat tgg tac ctg cag 528
 Ser Leu Val His Ser Asn Gly Lys Thr Tyr Leu His Trp Tyr Leu Gln
 165 170 175

aag cca ggc cag tct cca aaa ctc ctg atc tac aaa gtt tcc aac cga 576
 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
 180 185 190

ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca gtg aca gat 624
 Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Val Thr Asp
 195 200 205

ttc aca ctc atg atc agc aga gtg gag gct gag gat ctg gga gtt tat 672
 Phe Thr Leu Met Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
 210 215 220

ttc tgc tct caa agt aca cat gtt ccg tac acg ttc gga ggg ggg acc 720
 Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr
 225 230 235 240

aag ctg gaa ata aaa taatga 741
 Lys Leu Glu Ile Lys
 245

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<210> SEQ ID NO 30
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 30
cagacagtgg ttcaaagt 18

<210> SEQ ID NO 31
<211> LENGTH: 72
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 31
cgcgctgacc gatccgccac cacccgaacc accaccaccc gaaccaccac caccttttat 60
ttccagcttg gt 72

<210> SEQ ID NO 32
<211> LENGTH: 1605
<212> TYPE: DNA
<213> ORGANISM: Mus sp.
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1599)
<223> OTHER INFORMATION: pCHOM2(Fv)2. MABL2-sc(Fv)2

<400> SEQUENCE: 32
atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt 48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15
gtc gac tcc cag gtc cag ctg cag cag tct gga cct gaa ctg gta aag 96
Val Asp Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
 20 25 30
cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga tac acc ttc 144
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
gct aac cat gtt att cac tgg gtg aag cag aag cca ggg cag ggc ctt 192
Ala Asn His Val Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
 50 55 60
gag tgg att gga tat att tat cct tac aat gat ggt act aag tat aat 240
Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
 65 70 75 80
gag aag ttc aag gac aag gcc act ctg act tca gac aaa tcc tcc acc 288
Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Thr
 85 90 95
aca gcc tac atg gac ctc agc agc ctg gcc tct gag gac tct gcg gtc 336
Thr Ala Tyr Met Asp Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val
 100 105 110
tat tac tgt gca aga ggg ggt tac tat act tac gac gac tgg ggc caa 384
Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Thr Tyr Asp Asp Trp Gly Gln
 115 120 125
ggc acc act ctc aca gtc tcc tca ggt ggt ggt ggt tcc ggt ggt ggt 432
Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 130 135 140
ggg tcc ggt ggt ggc gga tcc gat gtt gtg atg acc caa agt cca ctc 480
Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser Pro Leu
 145 150 155 160
tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tca 528

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agt ggc agt gga tca gtg aca gat ttc aca ctc atg atc agc aga gtg      1488
Ser Gly Ser Gly Ser Val Thr Asp Phe Thr Leu Met Ile Ser Arg Val
                               485                               490                               495

gag gct gag gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt      1536
Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val
                               500                               505                               510

ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa gac tac aaa      1584
Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys
                               515                               520                               525

gac gat gac gat aaa taatga                                          1605
Asp Asp Asp Asp Lys
    530

<210> SEQ ID NO 33
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 33
tgaggaattc ccaccatggg atg                                          23

<210> SEQ ID NO 34
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 34
cacgacgtca ctcgagactg tgagagtggg gccttgccc                          40

<210> SEQ ID NO 35
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 35
agtctcgagt gacgtcgtga tgacccaaag tccactctcc                        40

<210> SEQ ID NO 36
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 36
gactggatcc tcattattta tcgtcatcgt c                                  31

<210> SEQ ID NO 37
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 37
cgcgtaatac gactcactat ag                                          22

<210> SEQ ID NO 38
<211> LENGTH: 46

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 38

gcaattggac ctgttttata tcgagcttgg tccccctcc gaactg 46

<210> SEQ ID NO 39
<211> LENGTH: 45
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 39

gctcgagata aaacaggtcc aattgcagca gtctggacct gaact 45

<210> SEQ ID NO 40
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 40

gactggatcc tcattattta tcgtcatcgt cttttagtgc tggaggact gtgagagtgg 60

<210> SEQ ID NO 41
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 41

gactgaattc ccaccatgaa gttgcctgtt ag 32

<210> SEQ ID NO 42
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 42

cagtctcgag tggtggttcc gacgtcgtga tgacccaag 40

<210> SEQ ID NO 43
<211> LENGTH: 43
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 43

cagtctcgag tggtggtggt tccgacgtcg tgatgacca aag 43

<210> SEQ ID NO 44
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 44

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cagtctcgag tgggtggtggt ggttccgacg tcgtgatgac ccaaag 46

<210> SEQ ID NO 45
 <211> LENGTH: 49
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 <400> SEQUENCE: 45

cagtctcgag tgggtggtggt ggtggttccg acgtcgtgat gacccaaag 49

<210> SEQ ID NO 46
 <211> LENGTH: 52
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 <400> SEQUENCE: 46

cagtctcgag tgggtggtggt ggtggtggtt cgcacgtcgt gatgacccaa ag 52

<210> SEQ ID NO 47
 <211> LENGTH: 20
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 <400> SEQUENCE: 47

ggccgcatgt tgtcacgaat 20

<210> SEQ ID NO 48
 <211> LENGTH: 780
 <212> TYPE: DNA
 <213> ORGANISM: Mus sp.
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(768)
 <223> OTHER INFORMATION: CF2HL-0/pCOS1. MABL2-scFv<HL-0>
 <400> SEQUENCE: 48

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt 48
 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15

gtc gac tcc cag gtc cag ctg cag cag tct gga cct gaa ctg gta aag 96
 Val Asp Ser Gln Val Gln Leu Gln Ser Gly Pro Glu Leu Val Lys
 20 25 30

cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga tac acc ttc 144
 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

gct aac cat gtt att cac tgg gtg aag cag aag cca ggg cag ggc ctt 192
 Ala Asn His Val Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
 50 55 60

gag tgg att gga tat att tat cct tac aat gat ggt act aag tat aat 240
 Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
 65 70 75 80

gag aag ttc aag gac aag gcc act ctg act tca gac aaa tcc tcc acc 288
 Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Thr
 85 90 95

aca gcc tac atg gac ctc agc agc ctg gcc tct gag gac tct gcg gtc 336
 Thr Ala Tyr Met Asp Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val
 100 105 110

tat tac tgt gca aga ggg ggt tac tat act tac gac gac tgg ggc caa 384

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Tyr	Tyr	Cys	Ala	Arg	Gly	Gly	Tyr	Tyr	Thr	Tyr	Asp	Asp	Trp	Gly	Gln	
		115					120				125					
ggc	acc	act	ctc	aca	gtc	tcg	agt	gac	gtc	gtg	atg	acc	caa	agt	cca	432
Gly	Thr	Thr	Leu	Thr	Val	Ser	Ser	Asp	Val	Val	Met	Thr	Gln	Ser	Pro	
	130					135				140						
ctc	tcc	ctg	cct	gtc	agt	ctt	gga	gat	caa	gcc	tcc	atc	tct	tgc	aga	480
Leu	Ser	Leu	Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	
145				150					155						160	
tca	agt	cag	agc	ctt	gtg	cac	agt	aat	gga	aag	acc	tat	tta	cat	tgg	528
Ser	Ser	Gln	Ser	Leu	Val	His	Ser	Asn	Gly	Lys	Thr	Tyr	Leu	His	Trp	
			165					170						175		
tac	ctg	cag	aag	cca	ggc	cag	tct	cca	aaa	ctc	ctg	atc	tac	aaa	gtt	576
Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	
		180						185						190		
tcc	aac	cga	ttt	tct	ggg	gtc	cca	gac	agg	ttc	agt	ggc	agt	gga	tca	624
Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	
	195					200				205						
gtg	aca	gat	ttc	aca	ctc	atg	atc	agc	aga	gtg	gag	gct	gag	gat	ctg	672
Val	Thr	Asp	Phe	Thr	Leu	Met	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	
	210					215				220						
gga	gtt	tat	ttc	tgc	tct	caa	agt	aca	cat	gtt	ccg	tac	acg	ttc	gga	720
Gly	Val	Tyr	Phe	Cys	Ser	Gln	Ser	Thr	His	Val	Pro	Tyr	Thr	Phe	Gly	
225				230					235					240		
ggg	ggg	acc	aag	ctg	gaa	ata	aaa	gac	tac	aaa	gac	gat	gac	gat	aaa	768
Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys	
			245					250						255		
taatgaggat	cc															780
<210> SEQ ID NO 49																
<211> LENGTH: 45																
<212> TYPE: DNA																
<213> ORGANISM: Artificial Sequence																
<220> FEATURE:																
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer																
<400> SEQUENCE: 49																
caagctcgag	ataaaatccg	gaggccaggt	ccaattgcag	cagtc												45
<210> SEQ ID NO 50																
<211> LENGTH: 48																
<212> TYPE: DNA																
<213> ORGANISM: Artificial Sequence																
<220> FEATURE:																
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer																
<400> SEQUENCE: 50																
caagctcgag	ataaaatccg	gaggtggcca	ggtccaattg	cagcagtc												48
<210> SEQ ID NO 51																
<211> LENGTH: 51																
<212> TYPE: DNA																
<213> ORGANISM: Artificial Sequence																
<220> FEATURE:																
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer																
<400> SEQUENCE: 51																
caagctcgag	ataaaatccg	gaggtgggtg	ccaggtccaa	ttgcagcagt	c											51
<210> SEQ ID NO 52																
<211> LENGTH: 54																
<212> TYPE: DNA																
<213> ORGANISM: Artificial Sequence																
<220> FEATURE:																

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<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 52

caagctcgag ataaaatccg gaggtggtgg tggccaggtc caattgcagc agtc 54

<210> SEQ ID NO 53

<211> LENGTH: 57

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 53

caagctcgag ataaaatccg gaggtggtgg tggggccag gtccaattgc agcagtc 57

<210> SEQ ID NO 54

<211> LENGTH: 780

<212> TYPE: DNA

<213> ORGANISM: Mus sp.

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(768)

<223> OTHER INFORMATION: CF2LH-0/pCOS1. MABL2-scFv<LH-0>

<400> SEQUENCE: 54

atg aag ttg cct gtt agg ctg ttg gtg ctg atg ttc tgg att cct ggt 48
Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Gly
1 5 10 15

tcc agc agt gat gtt gtg atg acc caa agt cca ctc tcc ctg cct gtc 96
Ser Ser Ser Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val
20 25 30

agt ctt gga gat caa gcc tcc atc tct tgc aga tca agt cag agc ctt 144
Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
35 40 45

gtg cac agt aat gga aag acc tat tta cat tgg tac ctg cag aag cca 192
Val His Ser Asn Gly Lys Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
50 55 60

ggc cag tct cca aaa ctc ctg atc tac aaa gtt tcc aac cga ttt tct 240
Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
65 70 75 80

ggg gtc cca gac agg ttc agt ggc agt gga tca gtg aca gat ttc aca 288
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Val Thr Asp Phe Thr
85 90 95

ctc atg atc agc aga gtg gag gct gag gat ctg gga gtt tat ttc tgc 336
Leu Met Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
100 105 110

tct caa agt aca cat gtt ccg tac acg ttc gga ggg ggg acc aag ctc 384
Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
115 120 125

gag ata aaa cag gtc caa ttg cag cag tct gga cct gaa ctg gta aag 432
Glu Ile Lys Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
130 135 140

cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga tac acc ttc 480
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
145 150 155 160

gct aac cat gtt att cac tgg gtg aag cag aag cca ggg cag ggc ctt 528
Ala Asn His Val Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
165 170 175

gag tgg att gga tat att tat cct tac aat gat ggt act aag tat aat 576
Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
180 185 190

gag aag ttc aag gac aag gcc act ctg act tca gac aaa tcc tcc acc 624

-continued

Glu	Lys	Phe	Lys	Asp	Lys	Ala	Thr	Leu	Thr	Ser	Asp	Lys	Ser	Ser	Thr	
	195						200					205				
aca	gcc	tac	atg	gac	ctc	agc	agc	ctg	gcc	tct	gag	gac	tct	gcg	gtc	672
Thr	Ala	Tyr	Met	Asp	Leu	Ser	Ser	Leu	Ala	Ser	Glu	Asp	Ser	Ala	Val	
	210					215				220						
tat	tac	tgt	gca	aga	ggg	ggg	tac	tat	act	tac	gac	gac	tgg	ggc	caa	720
Tyr	Tyr	Cys	Ala	Arg	Gly	Gly	Tyr	Tyr	Thr	Tyr	Asp	Asp	Trp	Gly	Gln	
225					230				235					240		
ggc	acc	act	ctc	aca	gtc	tcc	tca	gac	tac	aaa	gac	gat	gac	gat	aaa	768
Gly	Thr	Thr	Leu	Thr	Val	Ser	Ser	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys	
				245				250						255		
taatgaggat	cc															780

<210> SEQ ID NO 55
 <211> LENGTH: 18
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Linker peptide

<400> SEQUENCE: 55

Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Val
1				5					10					15	

Asp Ser

<210> SEQ ID NO 56
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Plasmid/linker nucleotide sequence
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(18)

<400> SEQUENCE: 56

gtc	tcg	agt	gac	gtc	gtg	18
Val	Ser	Ser	Asp	Val	Val	
1				5		

<210> SEQ ID NO 57
 <211> LENGTH: 6
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Plasmid/linker peptide sequence

<400> SEQUENCE: 57

Val	Ser	Ser	Asp	Val	Val
1				5	

<210> SEQ ID NO 58
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Plasmid/linker nucleotide sequence
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(27)

<400> SEQUENCE: 58

-continued

```

gtc tcg agt ggt ggt tcc gac gtc gtg
Val Ser Ser Gly Gly Ser Asp Val Val
  1             5

```

27

```

<210> SEQ ID NO 59
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:
      Plasmid/linker peptide sequence

<400> SEQUENCE: 59

```

```

Val Ser Ser Gly Gly Ser Asp Val Val
  1             5

```

```

<210> SEQ ID NO 60
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:
      Plasmid/linker nucleotide sequence
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(30)

<400> SEQUENCE: 60

```

```

gtc tcg agt ggt ggt ggt tcc gac gtc gtg
Val Ser Ser Gly Gly Gly Ser Asp Val Val
  1             5             10

```

30

```

<210> SEQ ID NO 61
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:
      Plasmid/linker peptide sequence

<400> SEQUENCE: 61

```

```

Val Ser Ser Gly Gly Gly Ser Asp Val Val
  1             5             10

```

```

<210> SEQ ID NO 62
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:
      Plasmid/linker nucleotide sequence
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(33)

<400> SEQUENCE: 62

```

```

gtc tcg agt ggt ggt ggt ggt tcc gac gtc gtg
Val Ser Ser Gly Gly Gly Gly Ser Asp Val Val
  1             5             10

```

33

```

<210> SEQ ID NO 63
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:
      Plasmid/linker peptide sequence

<400> SEQUENCE: 63

```

-continued

```
Val Ser Ser Gly Gly Gly Gly Ser Asp Val Val
  1           5           10
```

```
<210> SEQ ID NO 64
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:
      Plasmid/linker nucleotide sequence
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(36)
```

```
<400> SEQUENCE: 64
```

```
gtc tcg agt ggt ggt ggt ggt tcc gac gtc gtc           36
Val Ser Ser Gly Gly Gly Gly Gly Ser Asp Val Val
  1           5           10
```

```
<210> SEQ ID NO 65
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:
      Plasmid/linker peptide sequence
```

```
<400> SEQUENCE: 65
```

```
Val Ser Ser Gly Gly Gly Gly Gly Ser Asp Val Val
  1           5           10
```

```
<210> SEQ ID NO 66
<211> LENGTH: 39
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:
      Plasmid/linker nucleotide sequence
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(39)
```

```
<400> SEQUENCE: 66
```

```
gtc tcg agt ggt ggt ggt ggt ggt tcc gac gtc gtc           39
Val Ser Ser Gly Gly Gly Gly Gly Ser Asp Val Val
  1           5           10
```

```
<210> SEQ ID NO 67
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:
      Plasmid/linker peptide sequence
```

```
<400> SEQUENCE: 67
```

```
Val Ser Ser Gly Gly Gly Gly Gly Ser Asp Val Val
  1           5           10
```

```
<210> SEQ ID NO 68
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:
      Plasmid/linker nucleotide sequence
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(18)
```

-continued

<400> SEQUENCE: 68

gag ata aaa cag gtc caa
 Glu Ile Lys Gln Val Gln
 1 5

18

<210> SEQ ID NO 69

<211> LENGTH: 6

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence:
Plasmid/linker peptide sequence

<400> SEQUENCE: 69

Glu Ile Lys Gln Val Gln
 1 5

<210> SEQ ID NO 70

<211> LENGTH: 27

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence:
Plasmid/linker nucleotide sequence

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(27)

<400> SEQUENCE: 70

gag ata aaa tcc gga ggc cag gtc caa
 Glu Ile Lys Ser Gly Gly Gln Val Gln
 1 5

27

<210> SEQ ID NO 71

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence:
Plasmid/linker peptide sequence

<400> SEQUENCE: 71

Glu Ile Lys Ser Gly Gly Gln Val Gln
 1 5

<210> SEQ ID NO 72

<211> LENGTH: 30

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence:
Plasmid/linker nucleotide sequence

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(30)

<400> SEQUENCE: 72

gag ata aaa tcc gga ggt ggc cag gtc caa
 Glu Ile Lys Ser Gly Gly Gly Gln Val Gln
 1 5 10

30

<210> SEQ ID NO 73

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence:
Plasmid/linker peptide sequence

-continued

<400> SEQUENCE: 73

Glu Ile Lys Ser Gly Gly Gly Gln Val Gln
 1 5 10

<210> SEQ ID NO 74

<211> LENGTH: 33

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence:
Plasmid/linker nucleotide sequence

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(33)

<400> SEQUENCE: 74

gag ata aaa tcc gga ggt ggt ggc cag gtc caa
 Glu Ile Lys Ser Gly Gly Gly Gln Val Gln
 1 5 10

33

<210> SEQ ID NO 75

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence:
Plasmid/linker peptide sequence

<400> SEQUENCE: 75

Glu Ile Lys Ser Gly Gly Gly Gln Val Gln
 1 5 10

<210> SEQ ID NO 76

<211> LENGTH: 36

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence:
Plasmid/linker nucleotide sequence

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(36)

<400> SEQUENCE: 76

gag ata aaa tcc gga ggt ggt ggt ggc cag gtc caa
 Glu Ile Lys Ser Gly Gly Gly Gly Gly Gln Val Gln
 1 5 10

36

<210> SEQ ID NO 77

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence:
Plasmid/linker peptide sequence

<400> SEQUENCE: 77

Glu Ile Lys Ser Gly Gly Gly Gly Gln Val Gln
 1 5 10

<210> SEQ ID NO 78

<211> LENGTH: 39

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence:
Plasmid/linker nucleotide sequence

<220> FEATURE:

<221> NAME/KEY: CDS

-continued

<222> LOCATION: (1) .. (39)

<400> SEQUENCE: 78

```

gag ata aaa tcc gga ggt ggt ggt ggt ggc cag gtc caa      39
Glu Ile Lys Ser Gly Gly Gly Gly Gly Gly Gln Val Gln
  1             5             10

```

<210> SEQ ID NO 79

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence:
Plasmid/linker peptide sequence

<400> SEQUENCE: 79

```

Glu Ile Lys Ser Gly Gly Gly Gly Gly Gln Val Gln
  1             5             10

```

<210> SEQ ID NO 80

<211> LENGTH: 4

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Linker
peptide

<400> SEQUENCE: 80

```

Gly Gly Gly Ser
  1

```

<210> SEQ ID NO 81

<211> LENGTH: 4

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Linker
peptide

<400> SEQUENCE: 81

```

Ser Gly Gly Gly
  1

```

<210> SEQ ID NO 82

<211> LENGTH: 5

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Linker
peptide

<400> SEQUENCE: 82

```

Gly Gly Gly Gly Ser
  1             5

```

<210> SEQ ID NO 83

<211> LENGTH: 5

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Linker
peptide

<400> SEQUENCE: 83

```

Ser Gly Gly Gly Gly
  1             5

```

-continued

<210> SEQ ID NO 84
 <211> LENGTH: 6
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Linker
 peptide

<400> SEQUENCE: 84

Gly Gly Gly Gly Gly Ser
 1 5

<210> SEQ ID NO 85
 <211> LENGTH: 6
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Linker
 peptide

<400> SEQUENCE: 85

Ser Gly Gly Gly Gly Gly
 1 5

<210> SEQ ID NO 86
 <211> LENGTH: 7
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Linker
 peptide

<400> SEQUENCE: 86

Gly Gly Gly Gly Gly Gly Ser
 1 5

<210> SEQ ID NO 87
 <211> LENGTH: 7
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Linker
 peptide

<400> SEQUENCE: 87

Ser Gly Gly Gly Gly Gly Gly
 1 5

<210> SEQ ID NO 88
 <211> LENGTH: 15
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Linker
 peptide
 <220> FEATURE:
 <223> OTHER INFORMATION: this sequence may encompass 5-15 residues; for
 preferred embodiments see specification as filed

<400> SEQUENCE: 88

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10 15

<210> SEQ ID NO 89
 <211> LENGTH: 15
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Linker

-continued

peptide
 <220> FEATURE:
 <223> OTHER INFORMATION: this sequence may encompass 5-15 residues; for preferred embodiments see specification as filed

<400> SEQUENCE: 89

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 1 5 10 15

<210> SEQ ID NO 90
 <211> LENGTH: 131
 <212> TYPE: PRT
 <213> ORGANISM: Mus sp.
 <220> FEATURE:
 <223> OTHER INFORMATION: pGEM-M1L

<400> SEQUENCE: 90

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
 -15 -10 -5

Ser Ser Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val
 -1 1 5 10

Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
 15 20 25

Leu His Ser Lys Gly Asn Thr Tyr Leu Gln Trp Tyr Leu Gln Lys Pro
 30 35 40 45

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
 50 55 60

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 65 70 75

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
 80 85 90

Ser Gln Ser Thr His Val Pro Tyr Thr Ser Gly Gly Gly Thr Lys Leu
 95 100 105

Glu Ile Lys
 110

<210> SEQ ID NO 91
 <211> LENGTH: 136
 <212> TYPE: PRT
 <213> ORGANISM: Mus sp.
 <220> FEATURE:
 <223> OTHER INFORMATION: pGEM-M1H

<400> SEQUENCE: 91

Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
 -15 -10 -5

Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Asp Leu Val Lys
 -1 1 5 10

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 15 20 25

Val Asn His Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
 30 35 40 45

Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
 50 55 60

Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Glu Lys Ser Ser Ser
 65 70 75

Ala Ala Tyr Met Glu Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val
 80 85 90

Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Ser Tyr Asp Asp Trp Gly Gln

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```

          95              100              105
Gly Thr Thr Leu Thr Val Ser Ser
110                      115

<210> SEQ ID NO 92
<211> LENGTH: 131
<212> TYPE: PRT
<213> ORGANISM: Mus sp.
<220> FEATURE:
<223> OTHER INFORMATION: pGEM-M2L

<400> SEQUENCE: 92
Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Gly
          -15              -10              -5
Ser Ser Ser Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val
          -1  1              5              10
Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
          15              20              25
Val His Ser Asn Gly Lys Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
          30              35              40              45
Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
          50              55              60
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Val Thr Asp Phe Thr
          65              70              75
Leu Met Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
          80              85              90
Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
          95              100              105

Glu Ile Lys
110

<210> SEQ ID NO 93
<211> LENGTH: 136
<212> TYPE: PRT
<213> ORGANISM: Mus sp.
<220> FEATURE:
<223> OTHER INFORMATION: pGEM-M2H

<400> SEQUENCE: 93
Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
          -15              -10              -5
Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
          -1  1              5              10
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
          15              20              25
Ala Asn His Val Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
          30              35              40              45
Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
          50              55              60
Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Thr
          65              70              75
Thr Ala Tyr Met Asp Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val
          80              85              90
Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Thr Tyr Asp Asp Trp Gly Gln
          95              100              105

Gly Thr Thr Leu Thr Val Ser Ser
110                      115

```

-continued

<210> SEQ ID NO 94
 <211> LENGTH: 15
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Linker peptide

<400> SEQUENCE: 94

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10 15

<210> SEQ ID NO 95
 <211> LENGTH: 271
 <212> TYPE: PRT
 <213> ORGANISM: Mus sp.
 <220> FEATURE:
 <223> OTHER INFORMATION: pscM1. MABL1-scFv

<400> SEQUENCE: 95

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
 1 5 10 15
 Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Gln Ser Gly Pro Asp
 20 25 30
 Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
 35 40 45
 Tyr Thr Phe Val Asn His Val Met His Trp Val Lys Gln Lys Pro Gly
 50 55 60
 Gln Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr
 65 70 75 80
 Lys Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Glu Lys
 85 90 95
 Ser Ser Ser Ala Ala Tyr Met Glu Leu Ser Ser Leu Ala Ser Glu Asp
 100 105 110
 Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Ser Tyr Asp Asp
 115 120 125
 Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser
 130 135 140
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
 145 150 155 160
 Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser
 165 170 175
 Cys Arg Ser Ser Gln Ser Leu Leu His Ser Lys Gly Asn Thr Tyr Leu
 180 185 190
 Gln Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr
 195 200 205
 Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
 210 215 220
 Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu
 225 230 235 240
 Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr
 245 250 255
 Ser Gly Gly Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp
 260 265 270

<210> SEQ ID NO 96
 <211> LENGTH: 271
 <212> TYPE: PRT

-continued

```

<213> ORGANISM: Mus sp.
<220> FEATURE:
<223> OTHER INFORMATION: pCHOM1. MABL1-scFv

<400> SEQUENCE: 96

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
  1           5           10           15
Val Asp Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Asp Leu Val Lys
           20           25           30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
           35           40           45
Val Asn His Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
           50           55           60
Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
           65           70           75           80
Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Glu Lys Ser Ser Ser
           85           90           95
Ala Ala Tyr Met Glu Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val
           100          105          110
Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Ser Tyr Asp Asp Trp Gly Gln
           115          120          125
Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
           130          135          140
Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu
           145          150          155          160
Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser
           165          170          175
Ser Gln Ser Leu Leu His Ser Lys Gly Asn Thr Tyr Leu Gln Trp Tyr
           180          185          190
Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser
           195          200          205
Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
           210          215          220
Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly
           225          230          235          240
Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Ser Gly Gly
           245          250          255
Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp Asp Lys
           260          265          270

```

```

<210> SEQ ID NO 97
<211> LENGTH: 274
<212> TYPE: PRT
<213> ORGANISM: Mus sp.
<220> FEATURE:
<223> OTHER INFORMATION: pscM2. MABL2-scFv

```

```

<400> SEQUENCE: 97

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
  1           5           10           15
Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Gln Ser Gly Pro Glu
           20           25           30
Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
           35           40           45
Tyr Thr Phe Ala Asn His Val Ile His Trp Val Lys Gln Lys Pro Gly
           50           55           60

```

-continued

Gln Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr
65 70 75 80

Lys Tyr Asn Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr Ser Asp Lys
85 90 95

Ser Ser Thr Thr Ala Tyr Met Asp Leu Ser Ser Leu Ala Ser Glu Asp
100 105 110

Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Thr Tyr Asp Asp
115 120 125

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser
130 135 140

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
145 150 155 160

Ser Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser
165 170 175

Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Lys Thr Tyr Leu
180 185 190

His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr
195 200 205

Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
210 215 220

Gly Ser Val Thr Asp Phe Thr Leu Met Ile Ser Arg Val Glu Ala Glu
225 230 235 240

Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr
245 250 255

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp
260 265 270

Asp Lys

<210> SEQ ID NO 98
<211> LENGTH: 271
<212> TYPE: PRT
<213> ORGANISM: Mus sp.
<220> FEATURE:
<223> OTHER INFORMATION: pCHOM2. MABL2-scFv

<400> SEQUENCE: 98

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val Asp Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
20 25 30

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Ala Asn His Val Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
50 55 60

Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
65 70 75 80

Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Thr
85 90 95

Thr Ala Tyr Met Asp Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Thr Tyr Asp Asp Trp Gly Gln
115 120 125

Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser Pro Leu

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145             150             155             160
Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser
                165                 170                 175

Ser Gln Ser Leu Val His Ser Asn Gly Lys Thr Tyr Leu His Trp Tyr
                180                 185                 190

Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser
                195                 200                 205

Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Val
                210                 215                 220

Thr Asp Phe Thr Leu Met Ile Ser Arg Val Glu Ala Glu Asp Leu Gly
225                 230                 235                 240

Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly
                245                 250                 255

Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp Asp Lys
                260                 265                 270

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<210> SEQ ID NO 99
<211> LENGTH: 150
<212> TYPE: PRT
<213> ORGANISM: Mus sp.
<220> FEATURE:
<223> OTHER INFORMATION: pCHO-shIAP. Soluble human IAP

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<400> SEQUENCE: 99
Met Trp Pro Leu Val Ala Ala Leu Leu Leu Gly Ser Ala Cys Cys Gly
 1             5             10             15

Ser Ala Gln Leu Leu Phe Asn Lys Thr Lys Ser Val Glu Phe Thr Phe
                20             25             30

Cys Asn Asp Thr Val Val Ile Pro Cys Phe Val Thr Asn Met Glu Ala
 35             40             45

Gln Asn Thr Thr Glu Val Tyr Val Lys Trp Lys Phe Lys Gly Arg Asp
 50             55             60

Ile Tyr Thr Phe Asp Gly Ala Leu Asn Lys Ser Thr Val Pro Thr Asp
 65             70             75             80

Phe Ser Ser Ala Lys Ile Glu Val Ser Gln Leu Leu Lys Gly Asp Ala
 85             90             95

Ser Leu Lys Met Asp Lys Ser Asp Ala Val Ser His Thr Gly Asn Tyr
 100            105            110

Thr Cys Glu Val Thr Glu Leu Thr Arg Glu Gly Glu Thr Ile Ile Glu
 115            120            125

Leu Lys Tyr Arg Val Val Ser Trp Phe Ser Pro Asn Glu Asn Asp Tyr
 130            135            140

Lys Asp Asp Asp Asp Lys
145             150

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<210> SEQ ID NO 100
<211> LENGTH: 245
<212> TYPE: PRT
<213> ORGANISM: Mus sp.
<220> FEATURE:
<223> OTHER INFORMATION: pscM2DEm02. MABL2-scFv

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<400> SEQUENCE: 100
Met Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly
 1             5             10             15

Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Asn
 20             25             30

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-continued

Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser Pro Leu
 145 150 155 160
 Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser
 165 170 175
 Ser Gln Ser Leu Val His Ser Asn Gly Lys Thr Tyr Leu His Trp Tyr
 180 185 190
 Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser
 195 200 205
 Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Val
 210 215 220
 Thr Asp Phe Thr Leu Met Ile Ser Arg Val Glu Ala Glu Asp Leu Gly
 225 230 235 240
 Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly
 245 250 255
 Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly Gly Gly Gly
 260 265 270
 Ser Gly Gly Gly Gly Ser Val Asp Ser Gln Val Gln Leu Gln Gln Ser
 275 280 285
 Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys
 290 295 300
 Ala Ser Gly Tyr Thr Phe Ala Asn His Val Ile His Trp Val Lys Gln
 305 310 315 320
 Lys Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn
 325 330 335
 Asp Gly Thr Lys Tyr Asn Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr
 340 345 350
 Ser Asp Lys Ser Ser Thr Thr Ala Tyr Met Asp Leu Ser Ser Leu Ala
 355 360 365
 Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Thr
 370 375 380
 Tyr Asp Asp Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly
 385 390 395 400
 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Asp Val Val
 405 410 415
 Met Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala
 420 425 430
 Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Lys
 435 440 445
 Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu
 450 455 460
 Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe
 465 470 475 480
 Ser Gly Ser Gly Ser Val Thr Asp Phe Thr Leu Met Ile Ser Arg Val
 485 490 495
 Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val
 500 505 510
 Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys
 515 520 525
 Asp Asp Asp Asp Lys
 530

<210> SEQ ID NO 102

<211> LENGTH: 256

<212> TYPE: PRT

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<213> ORGANISM: Mus sp.
<220> FEATURE:
<223> OTHER INFORMATION: CF2HL-0/pCOS1. MABL2-scFv<HL-0>

<400> SEQUENCE: 102

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
  1           5           10           15
Val Asp Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
  20           25           30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
  35           40           45
Ala Asn His Val Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
  50           55           60
Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
  65           70           75           80
Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Thr
  85           90           95
Thr Ala Tyr Met Asp Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val
  100          105          110
Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Thr Tyr Asp Asp Trp Gly Gln
  115          120          125
Gly Thr Thr Leu Thr Val Ser Ser Asp Val Val Met Thr Gln Ser Pro
  130          135          140
Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg
  145          150          155          160
Ser Ser Gln Ser Leu Val His Ser Asn Gly Lys Thr Tyr Leu His Trp
  165          170          175
Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val
  180          185          190
Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser
  195          200          205
Val Thr Asp Phe Thr Leu Met Ile Ser Arg Val Glu Ala Glu Asp Leu
  210          215          220
Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly
  225          230          235          240
Gly Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp Asp Lys
  245          250          255

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<210> SEQ ID NO 103
<211> LENGTH: 256
<212> TYPE: PRT
<213> ORGANISM: Mus sp.
<220> FEATURE:
<223> OTHER INFORMATION: CF2LH-0/pCOS1. MABL2-scFv<LH-0>

<400> SEQUENCE: 103

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Gly
  1           5           10           15
Ser Ser Ser Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val
  20           25           30
Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
  35           40           45
Val His Ser Asn Gly Lys Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
  50           55           60
Gly Gln Ser Pro Lys Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
  65           70           75           80

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-continued

Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Val	Thr	Asp	Phe	Thr
				85					90					95	
Leu	Met	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val	Tyr	Phe	Cys
			100					105					110		
Ser	Gln	Ser	Thr	His	Val	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu
		115					120					125			
Glu	Ile	Lys	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val	Lys
	130					135					140				
Pro	Gly	Ala	Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
145					150					155					160
Ala	Asn	His	Val	Ile	His	Trp	Val	Lys	Gln	Lys	Pro	Gly	Gln	Gly	Leu
				165				170						175	
Glu	Trp	Ile	Gly	Tyr	Ile	Tyr	Pro	Tyr	Asn	Asp	Gly	Thr	Lys	Tyr	Asn
		180						185					190		
Glu	Lys	Phe	Lys	Asp	Lys	Ala	Thr	Leu	Thr	Ser	Asp	Lys	Ser	Ser	Thr
		195					200					205			
Thr	Ala	Tyr	Met	Asp	Leu	Ser	Ser	Leu	Ala	Ser	Glu	Asp	Ser	Ala	Val
	210					215					220				
Tyr	Tyr	Cys	Ala	Arg	Gly	Gly	Tyr	Tyr	Thr	Tyr	Asp	Asp	Trp	Gly	Gln
225					230					235					240
Gly	Thr	Thr	Leu	Thr	Val	Ser	Ser	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys
				245					250					255	

What is claimed is:

1. A reconstructed antibody which binds to Integrin Associated Protein (IAP), induces apoptosis of nucleated blood cells and causes no hemagglutination, wherein the reconstructed antibody comprises SEQ. ID NO. 101, or dimer of a sequence selected from SEQ ID NO. 95, SEQ ID NO. 96, SEQ ID NO. 97, SEQ ID NO. 98, SEQ ID NO. 100, SEQ ID NO. 102, or SEQ ID NO. 103.

2. A therapeutic agent for blood dyscrasia which comprises the reconstructed antibody of claim 1.

3. The therapeutic agent of claim 2, wherein the blood dyscrasia is leukemia.

4. The reconstructed antibody of claim 1, wherein the reconstructed antibody comprises a dimer of SEQ ID NO. 95.

5. The reconstructed antibody of claim 1, wherein the reconstructed antibody comprises a dimer of SEQ ID NO. 96.

6. The reconstructed antibody of claim 1, wherein the reconstructed antibody comprises a dimer of SEQ ID NO. 97.

7. The reconstructed antibody of claim 1, wherein the reconstructed antibody comprises a dimer of SEQ ID NO. 98.

8. The reconstructed antibody of claim 1, wherein the reconstructed antibody comprises a dimer of SEQ ID NO. 100.

9. The reconstructed antibody of claim 1, wherein the reconstructed antibody comprises SEQ ID NO. 101.

10. The reconstructed antibody of claim 1, wherein the reconstructed antibody comprises a dimer of SEQ ID NO. 102.

11. The reconstructed antibody of claim 1, wherein the reconstructed antibody comprises a dimer of SEQ ID NO. 103.

12. The therapeutic agent of claim 2, wherein the reconstructed antibody comprises a dimer of SEQ ID NO. 95.

13. The therapeutic agent of claim 2, wherein the reconstructed antibody comprises a dimer of SEQ ID NO. 96.

14. The therapeutic agent of claim 2, wherein the reconstructed antibody comprises a dimer of SEQ ID NO. 97.

15. The therapeutic agent of claim 2, wherein the reconstructed antibody comprises a dimer of SEQ ID NO. 98.

16. The therapeutic agent of claim 2, wherein the reconstructed antibody comprises a dimer of SEQ ID NO. 100.

17. The therapeutic agent of claim 2, wherein the reconstructed antibody comprises SEQ ID NO. 101.

18. The therapeutic agent of claim 2, wherein the reconstructed antibody comprises a dimer of SEQ ID NO. 102.

19. The therapeutic agent of claim 2, wherein the reconstructed antibody comprises a dimer of SEQ ID NO. 103.

* * * * *